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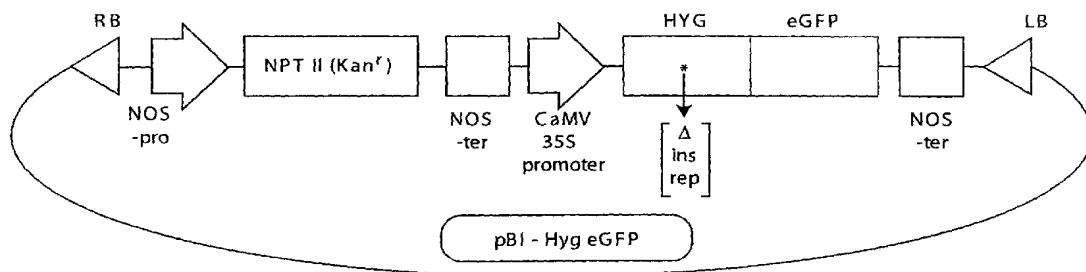
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.



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TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

Background Of The Invention

A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be

exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

5 More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Patent
10 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene
15 alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide.
20 Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of
25 these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such
30 chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., Nature 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat.

Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, Gene 24:107-116 (1997); Frary & Hamilton, Transgenic Res. 10: 121-132 (2001)).

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both *in vitro* using a cell-free extract assay and *in vivo* using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins *in vivo*, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein,

oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including; for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., *J. Am. Chem. Soc.*, 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications United States application no. 60/208,538, United States application no. 60/244,989, United States application no. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., *Nucleic Acids Research* 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-

LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koshkin, WO 01/25478 also allow specific targeted alteration of genetic information.

5 The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an *in vitro* gene repair assay. Similar results are also observed *in vivo* using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

25 **Detailed Description Of The Invention**

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration,

including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

Original codons*	Corresponding stop codon
<u>G</u> GGA (glycine), A GA (arginine), <u>C</u> GA (arginine), <u>T</u> TA (leucine), T <u>C</u> A (serine), T <u>G</u> I (cysteine), T <u>G</u> <u>G</u> (tryptophan), T <u>G</u> <u>C</u> (cysteine)	TGA
A AG (lysine), <u>G</u> AG (glutamate), <u>C</u> AG (glutamine), <u>T</u> IG (leucine), T <u>C</u> G (serine), T <u>G</u> <u>G</u> (tryptophan), T <u>A</u> I (cysteine), T <u>A</u> <u>C</u> (tyrosine)	TAG
A AA (lysine), <u>G</u> AA (glutamate), <u>C</u> AA (glutamine), <u>T</u> TA (leucine), T <u>C</u> A (serine), T <u>A</u> I (cysteine), T <u>A</u> <u>C</u> (tyrosine)	TAA

*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-
5 nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain
10 surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides
15 of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae*, *Ustilago maydis*, *Candida albicans*, and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and
20 *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as
25 walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichorium*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot
30 (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds,

such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins

involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having

phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desired change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery

which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

5 The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include
10 any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in
15 the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded
20 hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any
25 particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric
30 RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the

same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

5 The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or
10 gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241)
15 (<http://www.idtdna.com>); this program is available for use on the world wide web at

[http://www.idtdna.com/program/oligoanalyzer/
oligoanalyzer.asp](http://www.idtdna.com/program/oligoanalyzer/oligoanalyzer.asp).

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change
20 associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (<http://www.dnastar.com/products/PrimerSelect.html>).

25 If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle
30 between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed

strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

5 The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target
10 bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the
15 oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine
20 (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified *in vitro* or in another cell type, including for example, yeast or bacterial cells and then introduced
25 into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place *in vivo* following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

30 The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention

offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, RFLPs, AFLPs and CAPs.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA *in vitro* or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 µg/kg target tissue, preferably between 1 to 250 µg/kg, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve

efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

Brief Description Of The Drawings

Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

Figure 2. *Genetic readout system for correction of a point mutation in plasmid pK^sm4021.* A mutant kanamycin gene harbored in plasmid pK^sm4021 is the target for correction by oligonucleotides.

The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT^SΔ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan^r colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(+)FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a

base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function.

Figure 8. *Oligonucleotides for correction of hygromycin resistance gene*. The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FIAsH plasmid*. This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. *pYESHyg(x)eGFP plasmid*. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

Figure 11. *pBI-HygeGFP plasmid*. This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1

Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^sm4021 (Figure 2) or the tetracycline gene of pT^sΔ208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FIAsH (Figure 9), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase

(kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FIAsh ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FIAsh fusion product (after alteration) or the truncated Neo-/FIAsh product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in Figures 7B, 9 and 10 herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl.Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'-GACCTATCCACGCCCTCC-3'), Hyg Δ r (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrepf (5'-CTGGGATAGGTCCTGCGG-3'), Hyg Δ f

(5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'), respectively to primer HygEGFP_r (5'-AAATCACGCCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 µg of vector pHYGeGFP and 5 µg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper *et al.*, *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 µg/ml per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

Cell-free extracts. Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C1271 (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2×10^8 cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000xg. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage.

We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000xg for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000xg for 15 minutes. We then add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM MgCl₂, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H₂O, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10⁵ dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10⁻⁵ to correct for the amp dilution.

The following procedure can also be used. 5 µl of resuspended reaction mixtures (total volume 50 µl) are used to transform 20 µl aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 µg/ml kanamycin or 12 µg/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 µl of SOC. 100 µl aliquots are plated onto kan or tet agar plates and 100 µl of a 10⁻⁴ dilution of the cultures are concurrently plated on agar plates containing 100 µg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in

the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the exemplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO₂ in a humidified incubator to a density of 2 x 10⁵ cells/ml in an 8 chamber slide (Lab-Tek). After replacing the

regular DMEM with Optimem, the cells are co-transfected with 10 µg of plasmid pAURNeo(-)FIAsH and 5 µg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 µg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FIAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FIAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan^sm4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the pkan^sm4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion

activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^m4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT^sΔ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is

used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^sm4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence TTCGATAAGCCTATGCTGACCCGTG corrects the original mutation present in the kanamycin resistance gene of pK^sm4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence TTCGGCTACGACTGGGCACAACAGACAATTGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^sm4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^sM4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCCAGTCGTATCCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAA TAGCCTCTCCACCCAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-

GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK^sm4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl;

1.5 mM MgCl₂; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000 x *g* for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by
5 Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the
10 chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan ^r colonies	Fold increase
I	pK ^s m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^sm4021 (1 µg), the indicated oligonucleotide (1.5 µg chimeric oligonucleotide or 0.55 µg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 µg of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20µg sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A. Oligonucleotide	Plasmid	Extract	kan ^r colonies
IX (3S/25G)	↓	HUH7	637
X (6S/25G)		HUH7	836
IX		MEF2 ^{-/-}	781
X		MEF2 ^{-/-}	676
IX		MEF3 ^{-/-}	582
X		MEF3 ^{-/-}	530
IX		MEF ^{+/+}	332
X		MEF ^{+/+}	497
-		MEF2 ^{-/-}	10
-		MEF3 ^{-/-}	5
-		MEF ^{+/+}	14

Chimeric oligonucleotide (1.5 µg) or modified single-stranded oligonucleotide (0.55 µg) was incubated with 1 µg of plasmid pK^m4021 and 20 µg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2^{-/-}) or MSH3 (3^{-/-}) deleted. MEF^{+/+} indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet ^r colonies
Tet IX (3S/25A; 0.5 µg)	pT ⁺ Δ208 (1 µg)	-	0
-	↓	20 µg	0
Tet IX (0.5 µg)		↓	48
Tet IX (1.5 µg)			130
Tet IX (2.0 µg)			68
Tet I (chimera; 1.5 µg)	↓	↓	48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide.

The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10⁶ ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT⁺Δ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan ^r colonies
II (chimera)	pK ^S m4021	30μg Canola	337
IX (3S/25G)	↓	Canola	763
X (6S/25G)		Canola	882
II		<i>Musa</i>	203
IX		<i>Musa</i>	343
X		<i>Musa</i>	746
-		Canola	0
-		<i>Musa</i>	0
IX		- Canola	0
X		- <i>Musa</i>	0

Canola or *Musa* cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 μg) and modified single-stranded oligonucleotides IX and X (0.55μg) were used to correct pK^Sm4021. Total number of kan^r colonies are present per 10⁷ ampicillin resistant colonies and represent an average of four independent experiments.

Table V
Gene repair activity in cell-free extracts prepared from yeast (Saccharomyces cerevisiae)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	kan ^r /amp ^r x 10 ⁶
Wild type	pKan ^r m4021	1µg		0.36
Wild type	↓		1µg	0.81
ΔRAD52		1µg		10.72
ΔRAD52			1µg	17.41
ΔPMS1		1µg		2.02
ΔPMS1			1µg	3.23

In this experiment, the kan^r gene in pKan^r4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2

Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μ g pAUR123 vector DNA, as well as, 10 μ g of each pHyg(x)EGFP construct with KpnI and Sall (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74 α , is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence.

Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-O-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferably the 3' terminus) may be used in different embodiments.

Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT α at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD₆₀₀ was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 μ l 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μ l of cells with 5 μ g of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μ F, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200 μ l of this culture on selective plates containing 300 μ g/ml hygromycin and spread 200 μ l of a 10⁵ dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10⁵ aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells

containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-CTCGTGCTTTTCAGCTTCGATGTAGGAGGGCGTGG**G**TAC**G**TCCTGCGGGTAAATAGCTGCGCCGATG GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAA**A**CAGCTGCGCCGATG GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGTGCTTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAATAGCTGCGCCG**A**C**G** GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74 α , with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μ g, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74 α and HygE3T/74).

Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74 α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μ g. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10 ⁵)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide Tested (5 µg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (µg)	Colonies on hygromycin	Colonies on aureobasidin (/10 ⁵)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3 Cultured Cell Manipulation

Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either

the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin⁻CD38⁻ cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 µg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 µg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 µg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPES buffer and 50 µM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 µg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 µm to 0.3 µm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are fluorescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

For *in vitro* erythropoiesis from Lin⁻CD38⁻ cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythroid progeny. CD34⁺ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β-globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids,

liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

5 Biolistic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH₂PO₄, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or 10 comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl₂ is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously on a vortex mixer for 10 min at room 15 temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macro-projectile which is used to bombard each plate once at 900 psi (1 psi = 6.89 kPa) with a gap distance (distance from power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target 20 material) of 10 cm.

An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N₆ medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl₂ and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

30 Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use

about 3×10^5 protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

EXAMPLE 4

Plant Cells

5 The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific
10 site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon

. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations
15 can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 11, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene PulserTM). Competent *A. tumefaciens* is prepared using a method similar to that of
20 preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25 μ F, 200 Ω and 2.5 kV.

A. tumefaciens containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform
25 Arabidopsis by vacuum infiltration or by dipping flowers in an *Agrobacterium* solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, *Agrobacterium* can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

All publications and patent applications cited in this specification are herein incorporated
30 by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some

detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

5 **Notes on the tables presented below:**

Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

10 The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

15 The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

20 All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

25 The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

30 The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

Example 5**Engineering herbicide resistant plants**

Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonyleureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 10
Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGTCTGAGGTATATATCAC	4341
	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAGGCAGGAAGCTTAATAAGACCGGAGATTT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	4342
	GCTTCCTGCCTCCAAGT	4343
	ACTTGGAGGCAGGAAGC	4344
10 Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCGCATCCAAATCTCTCTCCAATCGGATCCTCC TTCTTGCCGCTCTATCTGAGGTACATATACT	4345
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTTGGATGCGGGTAGCTTAATGAGACCCGAGATTT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	4346
	GCTACCCGCATCCAAAT	4347
	ATTTGGATGCGGGTAGC	4348
15 Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTGCTTCTAAATCCCTTTCCAATCGTATTCTCC TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	4349
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTAGAAGCAGGCAATTTAACAGTGCCGTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	4350
	ATTGCCTGCTTCTAAAT	4351
	ATTTAGAAGCAGGCAAT	4352
20 Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTTGAATTGTCAGCA AGGGAGGCCTTCCCGCAGGGAAGGTAAAGCTCTCTGGATCAATT AGCAGCCAGTACTTGACTGCTCTGCTTATGGC	4353
	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTTACCTTCCCTGCGGGAAGGCCTCCCTTGCTGACAATTC GAACAGGAGGACATTTTCGTACCAAGGAAACAAT	4354
	CCTTCCCGCAGGGAAGG	4355
	CCTTCCCTGCGGGAAGG	4356
25 Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCACCTGTTTGTGTCAATGGAA TCGGAGGGCTACCTGCTGGCAAGGTCAAGCTGTCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4357
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGCCAGCAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	GCTACCTGCTGGCAAGG	4359
	CCTTGCCAGCAGGTAGC	4360
	ACTGTTTCCTTGGCACTGAATGCCACCTGTTCTGTCAAGGGA ATTGGAGGACTTCCTGCTGGCAAGGTTAAGCTCTCTGGTCCAT CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	4361
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCCTTGACAC GAACAGGTGGGCATTAGTGCCAAGGAAACAGT	4362
	ACTTCCTGCTGGCAAGG	4363
10	CCTTGCCAGCAGGAAGT	4364
	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTAGGCA CTGTAAATTGCCTGCTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACAACGT	4365
	ACAGTTGTTCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA GATAATGATTTAGAGCAGGCAATTTAACAGTGCCTGAAATCTCT TTAATGGGTTGCAACACTATCTCAGAAGGCT	4366
	ATTGCCTGCTCTAAAT	4367
	ATTTAGAGCAGGCAAT	4368
15	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTAAATTACCCGCTTCGAAATCCCTTTCCAATCGTATTCTCCT TCTTGCTGCCCTTTCTGAGGGAAGGACTGT	4369
	ACAGTCCTTCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTGGAAGCGGGTAATTTAACAGTACCAGATATATC TTTGATGGGTNCTAGCACAATCTCATGGGGTT	4370
	ATTACCCGCTTCGAAAT	4371
	ATTTGGAAGCGGGTAAT	4372
20	ATTGTTTCCTTGGCACTGACTGCCACCTGTTCTGKATCAACGGCA TTGGAGGGCTACCTGCTGGCAAGGTTAAGCTGTCTGGTCCATC AGCAGCCAATACTTGAGTTCCTTGCTGATGGC	4373
	GCCATCAGCAAGGAAGTCAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTTGCCAGCAGGTAGCCCTCCAATGCCGTTGATCG AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	4374
	GCTACCTGCTGGCAAGG	4375
	CCTTGCCAGCAGGTAGC	4376

Table 11
Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 10 Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCCTTGTAGCA ATCACAGGACAAGTCTCTCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4377
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4378
	GACAAGTCTCTCGTCGT	4379
	ACGACGAGAGACTTGTC	4380
15 Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCCTTGTAGCA ATCACAGGACAAGTCCAGCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4381
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGCTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4382
	ACAAGTCCAGCGTCGTC	4383
	TACGACGCTGGACTTGT	4384
20 Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCCTTGTAGCA ATCACAGGACAAGTCCAACGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	4385
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGTTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	4386
	ACAAGTCCAACGTCGTA	4387
	TACGACGTTGGACTTGT	4388
25 Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAACGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4389
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACC GTTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4390
	GATCCCGAACGGTGGCA	4391
	TGCCACC GTTCGGGATC	4392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAATGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	4393
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCATTTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	4394
	GATCCCGAATGGTGGCA	4395
	TGCCACCATTTCGGGATC	4396
10 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCCG CCATCACGGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4397
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4398
	GCCAGGTCTCCCGCCGC	4399
	GCGGCGGGAGACCTGGC	4400
15 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCCG CATCACGGGGCCAGGTCCAAACGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4401
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4402
	CCAGGTCCAAACGCCGCA	4403
	TGCGGCGTTGGACCTGG	4404
20 Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCCG CATCACGGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4405
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4406
	CCAGGTCCAGCGCCGCA	4407
	TGCGGCGCTGGACCTGG	4408
25 Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCTATGATCCCAAATGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4409
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4410
	GATCCCAAATGGGGGCG	4411

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCCCCATTTGGGATC	4412
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4413
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT GCCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	4414
	GACAGGTGTCGCGACGC	4415
	GCGTCGCGACACCTGTC	4416
Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4417
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	4418
	ACAGGTGCAGCGACGCA	4419
	TGCGTCGCTGCACCTGT	4420
Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCACACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4421
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4422
	GATCCCTAATGGTGGGG	4423
	CCCCACCATTAGGGATC	4424
Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAC	GGCCGTACCTCTTGGATATAATCGTCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	4425
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	4426
	GATCCCTAACGGTGGGG	4427
	CCCCACCGTTAGGGATC	4428
Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Ser CCG-TCG	TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTCTCGCGCCGCATGATCGGCACGGACGCC TTCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4429
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT GCCGATCATGCGGCGCGAGACCTGCCCGTGATGGCCACCATG GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	4430

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTCTCGCGCCGC	4431
	GCGGCGCGAGACCTGCC	4432
5 Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGTCCAGCGCCGCATGATCGGCACGGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4433
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCG TGCCGATCATGCGGCGCTGGACCTGCCCCGTGATGGCCACCATG GGGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	4434
	GCAGGTCCAGCGCCGCA	4435
	TGCGGCGCTGGACCTGC	4436
10 Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC	CTGGGCCATACTTGTGGATATCATCGTCCCTCACCAGGAGCATG TGCTGCCTATGATCCCTAACGGTGGTGCTTTCAAGGACATTATCA TGGAAGGTGATGGCAGGATTTCTGATTAAAC	4437
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGA AAGCACCACCGTAGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCCAG	4438
	GATCCCTAACGGTGGTG	4439
	CACCACCGTAGGGATC	4440
15 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGC CATCACGGGGCAGGTCTCACGCCGCATGATCGGCACGGACGCGT TCCAGGAGACGCCCATAGTGGAGGTCACGCGCT	4441
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTG CCGATCATGCGGCGTGAGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	4442
	GCCAGGTCTCACGCCGC	4443
	GCGGCGTGAGACCTGGC	4444
20 Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC ATCACGGGGCAGGTCCACGCCGCATGATCGGCACGGACGCGTT CCAGGAGACGCCCATAGTGGAGGTCACGCGCTC	4445
	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGT GCCGATCATGCGGCGTGGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	4446
	CCAGGTCCACGCCGCA	4447
	TGCGGCGTGGACCTGG	4448

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCCCGCATCAGGAGC ACGTGCTGCCTATGATCCCAA A CGGTGGTGCTTTCAAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA	4449
	TCAGTACGAGGTCCTGCCATCACCCCTCCATGATCATGTCCTTGAA AGCACCACCG T TTGGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	4450
	GATCCCAA A CGGTGGTG	4451
	CACCACCG T TTGGGATC	4452
10 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCT T CTCGTCGGATGATCGGTACCGATGCTTTC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	4453
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAG A GACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4454
	GTCAAGTCT T CTCGTCGG	4455
	CCGACGAG A GACTTGAC	4456
15 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC A ACGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	4457
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG T TGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4458
	TCAAGTCC A ACGTCGGA	4459
	TCCGACG T TGGACTTGA	4460
20 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC A ACGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	4461
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG C TGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4462
	TCAAGTCC A ACGTCGGA	4463
	TCCGACG C TGGACTTGA	4464
25 Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCA A TGGAGGCGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4465
	TGAGGTCAATATTGTGTTCTTCCATCACCCCTCTGTGATCACATCTT TGAAAGCGCCTCCA T TGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4466
	GATCCCCA A TGGAGGCG	4467

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGCCTCCA <u>T</u> TGGGGATC	4468
5 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCC ATTACTGGGCAAGTT <u>T</u> CCCGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGAT	4469
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG <u>A</u> AACCTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	4470
	GGCAAGTT <u>T</u> CCCGGCGT	4471
	ACGCCGGG <u>A</u> AACCTTGCC	4472
10 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>C</u> AACGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGATC	4473
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>T</u> TGAACCTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	4474
	GCAAGTT <u>C</u> AACGGCGTA	4475
	TACGCCG <u>T</u> TGAACCTTGC	4476
15 Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>C</u> AGCGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGATC	4477
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>C</u> TGAACCTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	4478
	GCAAGTT <u>C</u> AGCGGCGTA	4479
	TACGCCG <u>C</u> TGAACCTTGC	4480
25 Imidazolinone Resistance ALS <i>Amaranthus retroflexus</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>A</u> CGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4481
	ACCAACTAATAAGCCCTTCTTCCATCACCTCTGTTATGGTGTCTT TGAAGGCGGCACCG <u>T</u> AGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	4482
	GATCCCTA <u>A</u> CGGTGCCG	4483
	CGGCACCG <u>T</u> TAGGGATC	4484

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGAT	4485
	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	4486
	GTCAAGTGTCACGTAGG	4487
	CCTACGTGACACTTGAC	4488
10 Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGATC	4489
	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	4490
	TCAAGTGCAACGTAGGA	4491
	TCCTACGTGCACTTGGA	4492
15 Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTTCTATTGAGTTTG	4493
	CAAACCTCAATAGGAACCTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4494
	GATTCCCAATGGCGGAG	4495
	CTCCGCCATTGGGAATC	4496
20 Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAAGTAGAT	4497
	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT	4498
	GTCAAGTGTCACGTAGG	4499
	CCTACGTGACACTTGAC	4500
25 Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAAGTAGATC	4501
	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	4502
	TCAAGTGCAACGTAGGA	4503

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCTACGT <u>T</u> GCACTTGA	4504
5 Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT	GGCCATACTTGTGGATGTGATTGTACCTCATCAGGAACATGTTCT ACCTATGATTCCCA <u>A</u> TGGCGGGGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGACTTTG	4505
	CAAAGTCAATAGGAACCTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCCCCGCCA <u>T</u> TGGGAATCATAGGTAGAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	4506
	GATTCCCA <u>A</u> TGGCGGGG	4507
	CCCCGCCA <u>T</u> TGGGAATC	4508
10 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA TTACTGGTCAAGTT <u>T</u> CCAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTT	4509
	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGG <u>A</u> AACCTTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT	4510
	GTCAAGTT <u>T</u> CCAGGAGA	4511
	TCTCCTGG <u>A</u> AACCTTGAC	4512
15 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTCA <u>AA</u> AGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTT	4513
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC CAATCATTCTCCT <u>TT</u> GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4514
	TCAAGTTCA <u>AA</u> AGGAGAA	4515
	TTCTCCT <u>TT</u> GAACTTGA	4516
20 Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTCA <u>AG</u> AGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTT	4517
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC CAATCATTCTCCT <u>CT</u> GAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	4518
	TCAAGTTCA <u>AG</u> AGGAGAA	4519
	TTCTCCT <u>CT</u> GAACTTGA	4520
25 Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT	GGGCCTTACTTGTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCCCG <u>AA</u> TGGTGGAGGTTTCATGGATGTGATCACC GAAGGCGACGGCAGAATGAAATATTGAGCTT	4521
	AAGCTCAATATTTTATTCTGCCGTCGCCTTCGGTGATCACATCCAT GAAACCTCCACCA <u>TT</u> CGGGATCATGGGCAACACATGTTCTTGATG GGGCACGATCACATCCAACAAGTAAGGCC	4522

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	TGATCCCGAATGGTGGA	4523
	TCCACCATTCGGGATCA	4524
	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTGTCGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	4525
	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTGCGCGCGACACCTGCCCCGTGATCGCCACCAGTGGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	4526
	GGCAGGTGTCGCGGCGA	4527
10	TCGCGCGCGACACCTGCC	4528
	CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGCGACGCGCAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	4529
	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTGCGCGCTGCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	4530
	GCAGGTGCAGCGGCGAA	4531
	TTGCGCGCTGCACCTGC	4532
15	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCTAATGGTGCAGCCTTCAAGGATATCATTAACTA AGGTGATGGAAGAACAAGTTATTGATGTTT	4533
	GAACATCAATAACTTGTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCATTAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	4534
	GATTCCTAATGGTGCAG	4535
	CTGCACCATTAGGAATC	4536
20	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTTGTGCGC CATTACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGGT	4537
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGAAGGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	4538
	GACAGGTCTCTCGCCGG	4539
	CCGGCGAGAGACCTGTC	4540

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTGCGCC ATTACAGGACAGGTCC <u>A</u> ACGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4541
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG <u>T</u> TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACC CGC	4542
	ACAGGTCC <u>A</u> ACGCCGGA	4543
	TCCGGCG <u>T</u> TGGACCTGT	4544
10 Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTGCGCC ATTACAGGACAGGTCC <u>A</u> GCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGGTC	4545
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG <u>C</u> TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACC CGC	4546
	ACAGGTCC <u>A</u> GCGCCGGA	4547
	TCCGGCG <u>C</u> TGGACCTGT	4548
15 Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACAGA AGGGGATGGTGCCTAAGTACTGAGAGAT	4549
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTT TGAAAGTGCCACCA <u>T</u> TTGGGATCATCGGTAACACATGTTCTTGGT GCGGACATATCACATCCAACAGGTATGGTC	4550
	GATCCCAA <u>A</u> TGGTGGCA	4551
	TGCCACCA <u>T</u> TTGGGATC	4552
20 Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTGCG CCATTACAGGACAGGT <u>T</u> CCTCGCCGGATGATCGGTACTGACGCC TTCCAAGAGACACCAATCGTTGAGGTAACGAGG	4553
	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACC GATCATCCGGCGAGG <u>A</u> ACCTGTCCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACC CGCTG	4554
	GGACAGGT <u>T</u> CCTCGCCG	4555
	CGGCGAGG <u>A</u> ACCTGTCC	4556
25 Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Gln CCC-CAG	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTGCG CATTACAGGACAGGT <u>C</u> ACTCGCCGGATGATCGGTACTGACGCCT TCCAAGAGACACCAATCGTTGAGGTAACGAGGT	4557
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAG <u>T</u> GACCTGTCCTGTAATGGCGACAAGAGGA AACTGTCAAGCATCGCGTCTGCTAACC CGCT	4558
	GACAGGT <u>C</u> ACTCGCCG	4559

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CCGGCGAG <u>I</u> GACCTGTC	4560
Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACAGA AGGGGATGGTCGCACTAAGTACTGAGAGAT	4561
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTT TGAAAGTGCCACCA <u>TTT</u> GGGATCATCGGTAACACATGTTCTTGGT GCGGACATATCACATCCAACAGGTATGGTC	4562
	GATCCCAA <u>A</u> TGGTGGCA	4563
	TGCCACCA <u>TTT</u> GGGATC	4564
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGC CATCACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	4565
	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCCTGTGATGGCGACGAGAGGA ACACTGTCAAGCATCGCGTCGGCTAACCCGCT	4566
	GACAGGTCTCTCGCCGG	4567
	CCGGCGAG <u>A</u> GACCTGTC	4568
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>AA</u> CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4569
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>TT</u> GGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4570
	ACAGGTCC <u>AA</u> CGCCGGA	4571
	TCCGGCG <u>TT</u> GGACCTGT	4572
Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>AG</u> CGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	4573
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>CT</u> GGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	4574
	ACAGGTCC <u>AG</u> CGCCGGA	4575
	TCCGGCG <u>CT</u> GGACCTGT	4576
Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	4577
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCA <u>TTT</u> GGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC	4578

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	GATCCCAA <u>A</u> TGGTGGCA	4579
	TGCCACCA <u>T</u> TTGGGATC	4580
	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCG CCATCACGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGC CTTCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	4581
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG <u>A</u> GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	4582
10	GCCAGGTCTCCCGCCGC	4583
	GCGGCGGG <u>A</u> GACCTGGC	4584
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC <u>A</u> ACGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4585
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGT <u>T</u> GGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4586
15	CCAGGTCC <u>A</u> ACGCCGCA	4587
	TGCGGCGT <u>T</u> GGACCTGG	4588
	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCC <u>A</u> AGCGCCGCATGATCGGCACCGACGCC TTCCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	4589
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGC <u>T</u> GGACCTGGCCCGTGATGGCGACCATC GGGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	4590
20	CCAGGTCC <u>A</u> AGCGCCGCA	4591
	TGCGGCGC <u>T</u> GGACCTGG	4592
	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCTATGATCCCAA <u>A</u> TGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	4593
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA <u>T</u> TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	4594
	GATCCCAA <u>A</u> TGGGGGCG	4595
	CGCCCCCA <u>T</u> TTGGGATC	4596

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	4597
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTG CCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	4598
	GACAGGTGTCGCGACGC	4599
	GCGTCGCGACACCTGTC	4600
10 Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTT TCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	4601
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT GCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	4602
	ACAGGTGCAGCGACGCA	4603
	TGCGTCGCTGCACCTGT	4604
15 Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT	GGCCGTACCTCTTGATATAATCGTCCCGCACCAGGAGCATGTGT TGCCATATGATCCCTAATGGTGGGGCTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT	4605
	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGCC	4606
	GATCCCTAATGGTGGGG	4607
	CCCCACCATTAGGGATC	4608
20 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAACTCCAATTGTTGAGGTAACAAGGT	4609
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	4610
	GTCAAGTCTCTCGTCGG	4611
	CCGACGAGAGACTTGAC	4612
25 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAAACGTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4613
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4614
	TCAAGTCCAAACGTCGGA	4615

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCGACGTTGGACTTGA	4616
5 Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAGCGTCGGATGATCGGTACCGATGCTTTCC AGGAACTCCAATTGTTGAGGTAACAAGGTC	4617
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGCTGGACTTGACCAAGTATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	4618
	TCAAGTCCAGCGTCGGA	4619
	TCCGACGCTGGACTTGA	4620
10 Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCAATGGAGGGGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	4621
	TGAGGTCAATATTGTGTTCTTCCATCACCTCTGTGATCACATCTT TGAAAGCCCCCTCCATTGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	4622
	GATCCCCAATGGAGGGG	4623
	CCCCCTCCATTGGGGATC	4624
15 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCC ATTACTGGGCAAGTTTCCCGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGAT	4625
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGGAAGCTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAAGTGCATCAGCAAGACCAGA	4626
	GGCAAGTTTCCCGGCGT	4627
	ACGCCGGGAAGCTTGCC	4628
20 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGATC	4629
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGTTGAAGCTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAAGTGCATCAGCAAGACCAG	4630
	GCAAGTTCAACGGCGTA	4631
	TACGCCGTTGAAGCTTGC	4632
25 Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTC AAGAGACTCCAATTGTTGAGGTAACCTCGATC	4633
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGCTGAAGCTTGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAAGTGCATCAGCAAGACCAG	4634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCAAGTTC <u>AG</u> CGGCGTA	4635
	TACGCCG <u>CT</u> GAACTTGC	4636
Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>AC</u> GGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	4637
	ACCAACTAATAAGCCCTTCTTCCATCACCTCTGTTATGGTGTCTT TGAAGGCGGCACCG <u>IT</u> AGGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	4638
	GATCCCTA <u>AC</u> GGTGCCG	4639
	CGGCACCG <u>IT</u> AGGGATC	4640

Table 12
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 10 Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAACT ATATTACCCACCAATGGCAGCAGTATCTATCTCGTACCCGAAAGA AGCAATCCGAACAGAATGTTTGATAGATGG	4641
	CCATCTATCAAACATTCTGTTCCGATTGCTTCTTTCCGGTACGAGA TAGATACTGCTGCCATTGGTGGGTAATATAGTTTTGAGAGTGCATT TGCAGCAGATTGAGAAAGAGGGCGCAAGA	4642
	CCCACCAATGGCAGCAG	4643
	CTGCTGCCATTGGTGGG	4644
15 Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG	TATTACGTCTCTTTCCGTTGCCGCAGCAGATGCACTTTCAAATTT CTACTATCCCCCAATGGGAGCAGTCACAATTTTATATCCTCAAGAA GCTATTCGTGATGAGCGTCTGGTTGATGG	4645
	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCCCATTTGGGGGATAGTAAAAATTTGAAAGTGCA TCTGCTGCGGCAACCGAAAGAGGACGTAATA	4646
	TCCCCCAATGGGAGCAG	4647
	CTGCTCCCATTGGGGGA	4648
20 Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG	TGTTGCGTCCGCTTTTCGTTGGGTGCAGCAGATGCATTGTCAAAT TTTATTATCCTCCGATGGCAGCTGTATCAATTTTATATCCAAAAGA CGCAATTCGTGCTGACCGGCTGATTGATGG	4649
	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA ATTGATACAGCTGCCATTCGGAGGATAATAAAATTTTGAACATGCAT CTGCTGCACCCAACGAAAGCGGACGCAACA	4650
	TCCTCCGATGGCAGCTG	4651
	CAGCTGCCATTCGGAGGA	4652
25 Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG	TCCTTCGTCCACTTTTTCAGATGTCGCCGCAGAATCTCTTTCAAAT TCATTATCCACCAATGGCAGCTGTGTCACTTTTCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG	4653
	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA GTGACACAGCTGCCATTGGTGGATAATGAAATTTTGAAGAGATTCT TGCGGCGACATCTGAAAGTGGACGAAGGA	4654
	TCCACCAATGGCAGCTG	4655
	CAGCTGCCATTGGTGGA	4656

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATT CTATTATCCACCGATGGCTGCTGTAAGTGTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	4657
	CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAAC AGTTACAGCAGCCATCGGTGGATAATAGAATCTTGATAGAGCATC TGCAGCATCGCTTGAAAGTGGACGCAAAA	4658
	TCCACCGATGGCTGCTG	4659
	CAGCAGCCATCGGTGGA	4660
10 Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG	TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATT CTATTATCCACCAATGGCTGCTGTAAGTGTTCATATCCAAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	4661
	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCTTTGGATATGAAAC AGTTACAGCAGCCATTGGTGGATAATAGAATATTGACAGAGCATCT GCTGCATCACTTGAAAGTGGCCGCAAGA	4662
	TCCACCAATGGCTGCTG	4663
	CAGCAGCCATTGGTGGA	4664
15 Porphyric Herbicide Resistant PPO <i>Chlamydomonas reinhardtii</i> Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCCGCCGCGCCGAGGCCCTGGGCT CCTTCGACTACCCGCCGATGGGCGCCGTGACGCTGTCGTACCCG CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	4665
	CCGAGGCCCTTGCCTCCTCCCGCACGGCGCTCAGCGGGTACGA CAGCGTCACGGCGCCCATCGGCGGGTAGTCGAAGGAGCCCAGG GCCTCGGCGGCGGCGGGCGCCTGCTCCTTGACCAG	4666
	ACCCGCCGATGGGCGCC	4667
	GGCGCCCATCGGCGGGT	4668

Table 13
Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4669
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	ATATGCTA <u>C</u> TTTCAACA	4671
	TGTTGAAAGTAGCATAT	4672
	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4673
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4674
	ATATGCTA <u>C</u> TTTCAACA	4675
	TGTTGAAAGTAGCATAT	4676
10	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTTAACAACCTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4677
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4678
	ATATGCTA <u>C</u> TTTTAACA	4679
	TGTTAAAAGTAGCATAT	4680
15	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4681
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4682
	ATATGCTA <u>C</u> TTTCAACA	4683
	TGTTGAAAGTAGCATAT	4684
20	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCGTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4685
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4686
	ATATGCTA <u>C</u> TTTCAACA	4687
	TGTTGAAAGTAGCATAT	4688
25	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4689
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	4690
	ATATGCTA <u>C</u> TTTCAACA	4691

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGTTGAAAGTAGCATAT	4692
5 Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCAACTTTCAACAATTCTCGTTCTTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4693
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAGGTTT	4694
	ATATGCAACTTTCAACA	4695
	TGTTGAAAGTTGCATAT	4696
10 Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTTCAACAATTCTCGTTCTTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4697
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4698
	ATATGCTACTTTTCAACA	4699
	TGTTGAAAGTAGCATAT	4700
15 Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTACTTTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	4701
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	4702
	ATATGCTACTTTTCAACA	4703
	TGTTAAAAGTAGCATAT	4704
20 Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTACTTTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4705
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4706
	ATATGCTACTTTTCAACA	4707
	TGTTGAAAGTAGCATAT	4708
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTTCAACAATTCTCGTTCTTTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	4709
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4710
	ATATGCTACTTTTCAACA	4711
	TGTTGAAAGTAGCATAT	4712

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACCTCTCGTTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4713
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4714
	ATATGCTACTTTCAACA	4715
	TGTTGAAAGTAGCATAT	4716
10 Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTTAAACAACCTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	4717
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCGGCTACGATATTATAAGTTT	4718
	ATATGCTACTTTTAAACA	4719
	TGTTAAAAGTAGCATAT	4720
15 Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACCTCTCGTTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4721
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4722
	ATATGCTACTTTCAACA	4723
	TGTTGAAAGTAGCATAT	4724
20 Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4725
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4726
	ATATGCTACTTTCAACA	4727
	TGTTGAAAGTAGCATAT	4728
25 Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACCTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4729
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	4730
	ATATGCTACTTTCAACA	4731
	TGTTGAAAGTAGCATAT	4732

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCAAC <u>CTTT</u> CAACAATTCTCGTTCTTTACATTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTG	4733
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAG <u>GTT</u> GCATATTGGAAGATCAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAGGTTT	4734
	ATATGCAAC <u>CTTT</u> CAACA	4735
	TGTTGAAAG <u>GTT</u> GCATAT	4736
10 Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>ACTTTT</u> CAACAATTCTCGTTCTTTACATTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTG	4737
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4738
	ATATGCTA <u>ACTTTT</u> CAACA	4739
	TGTTGAAAG <u>G</u> TAGCATAT	4740
15 Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTA <u>CTTTT</u> AACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTG	4741
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAA <u>G</u> TAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	4742
	ATATGCTA <u>CTTTT</u> AACA	4743
	TGTTAAAA <u>G</u> TAGCATAT	4744
20 Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTA <u>CTTTT</u> CAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	4745
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATTAATCGACCAAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	4746
	ATATGCTA <u>CTTTT</u> CAACA	4747
	TGTTGAAAG <u>G</u> TAGCATAT	4748
25 Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTA <u>CTTTT</u> CAACAATTCTCGTTCTTTACATTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTG	4749
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4750
	ATATGCTA <u>CTTTT</u> CAACA	4751
	TGTTGAAAG <u>G</u> TAGCATAT	4752

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTTGCGCCGATTGAT CTTCCAGTATGCTA <u>C</u> TTTCAACAACCTCCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG	4753
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAGATCAATCGGCCGAAA TAACCGTGAGCAGCCACAATATTGTAGGTTT	4754
	GTATGCTA <u>C</u> TTTCAACA	4755
	TGTTGAAAGTAGCATAC	4756
10 Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4757
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATATTATAGGTTT	4758
	ATATGCTA <u>C</u> TTTCAACA	4759
	TGTTGAAAGTAGCATAT	4760
15 Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4761
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCCACAATATTATAAGTCT	4762
	ATATGCTACTTTCAACA	4763
	TGTTGAAAGTAGCATAT	4764
20 Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	4765
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCCACAATATTATAAGTTT	4766
	ATATGCTA <u>C</u> TTTCAACA	4767
	TGTTGAAAGTAGCATAT	4768
25 Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT	AAACTTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTAATC TTCCAATATGCA <u>A</u> CTTTCAACAATTCTCGTTCTTTACATTTCTTCT AGCTGCTTGGCCTGTAGTAGGTATTTG	4769
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAAGTTT	4770
	ATATGCA <u>A</u> CTTTCAACA	4771
	TGTTGAAAGTTGCATAT	4772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCAACTTTCAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTTGTAGGTATCTG	4773
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAGTTGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATATTATAGGTTT	4774
	ATATGCAACTTTCAACA	4775
	TGTTGAAAGTTGCATAT	4776
10 Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	4777
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	4778
	ATATGCTACTTTCAACA	4779
	TGTTGAAAGTAGCATAT	4780
15 Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4781
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATATTATAGGTTT	4782
	ATATGCTACTTTCAACA	4783
	TGTTGAAAGTAGCATAT	4784
20 Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGAT CTTCCAATATGCTACTTTCAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	4785
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGACCAAAT AACCATGAGCAGCTACGATATTATAAGTTT	4786
	ATATGCTACTTTCAACA	4787
	TGTTGAAAGTAGCATAT	4788
25 Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACCTCTCGTTCTTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4789
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAAT TAACCATGAGCGGCTACGATGTTATAAGTTT	4790
	ATATGCTACTTTCAACA	4791
	TGTTGAAAGTAGCATAT	4792

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4793
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	4794
	ATATGCTA <u>C</u> TTTCAACA	4795
	TGTTGAAAGTAGCATAT	4796
10 Triazine Resistant D1 Protein <i>Nicotiana plumbaginifolia</i> Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	4797
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	4798
	ATATGCTA <u>C</u> TTTCAACA	4799
	TGTTGAAAGTAGCATAT	4800

Example 6
Engineering male- or female-sterile plants

Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 14
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AP3 <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGA GAAGAATATGGCGTGAGGGAAGATCCAGATCAAGAGGATAGAGAA CCAGACAAACAGACAAGTGACGTATTCAA	4801
	TTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATC TGGATCTTCCCTCAGCCATATTCTTCTCTCTTTGTTAATCTTTTT GTTGAAGAGATTTGGTGGAGAGGACAA	4802
	ATATGGCGTGAGGGAAG	4803
	CTTCCCTCAGCCATAT	4804
Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGGTAGATCCAGATCAAGAGGATAGAGAACCAGA CAAACAGACAAGTGACGTATTCAAAGAGAA	4805
	TTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTC TTGATCTGGATCTACCCTCTCGCCATATTCTTCTCTCTTTGTTTAAT CTTTTTGTTGAAGAGATTTGGTGGAGA	4806
	CGAGAGGGTAGATCCAG	4807

	CTGGATCT <u>ACC</u> CTCTCG	4808
5	Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG	4809
	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAGATCTAGATCAAGAGGATAGAGAACCAGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG	4810
	CATTCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT ATCCTCTTGATCTAGATCTTCCCTCTCGCCATATTCTTCTCTCTTTG TTTAATCTTTTTGTTGAAGAGATTTGG	4811
	GGAAGATCTAGATCAAG	4812
	CTTGATCTAGATCTTCC	4813
10	Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG	4814
	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATCTAGAGGATAGAGAACCAGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTTAT	4815
	ATAAACCATTCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG TTCTCTATCCTCTAGATCTGGATCTTCCCTCTCGCCATATTCTTCTC TCTTTGTTTAATCTTTTTGTTGAAGAG	4816
	TCCAGATCTAGAGGATA	4817
	TATCCTCTAGATCTGGA	4818
15	Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG	4819
	AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGA CAAGTGACGTATTCTTAGAGAAGAAATGGTTTGTTCAGAAAGCTC ACGAGCTTACAGTTTTATGTGATGCTAGGG	4820
	CCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGAACAA ACCATTTCTTCTCTAGAATACGTCACTTGTCTGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTTCCCTCT	4821
	CGTATTCTTAGAGAAGA	4822
	TCTTCTCTAGAATACG	4823
20	Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA	4824
	GGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA GTGACGTATTCTAAGTGAAGAAATGGTTTGTTCAGAAAGCTCACG AGCTTACAGTTTTATGTGATGCTAGGGTTT	4825
	AAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGA CAAACCATTTCTTCACTTAGAATACGTCACTTGTCTGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTTCCC	4826
	ATTCTAAGTGAAGAAAT	4827
	ATTTCTTCACTTAGAAT	4828
25	Male-sterile AP3 <i>Brassica oleracea</i> Arg25Term AGA-TGA	4829
	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTG ACGTATTCTAAGAGATGAATGGTTTGTTCAGAAAGCTCACGAGC TTACAGTTTTATGTGATGCTAGGGTTTTCGA	4830
	TCGAAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTT GAACAAACCATTTCACTCTTAGAATACGTCACTTGTCTGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT	4831
	CTAAGAGATGAATGGT	4832
	ACCATTTCACTCTTAG	4833

5	Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTTAGTTCAAGAAAGCTCACGAGCTTACAGTTTT ATGTGATGCTAGGGTTTCGATTATCATGTT	4829
		AACATGATAATCGAAACCCTAGCATCACATAAACTGTAAGCTCGT GAGCTTTCTTGAACTAACCATTTCTTCTCTTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTCTATCCTCTTGA	4830
		AAATGGTTAGTTCAAGA	4831
		TCTTGAACTAACCATTT	4832
10	Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAAACAAA CAGGCAGGTCACCTAGTCCAAGAGAAGAAATGGTTTGTTCAAGAA AGCACACGAGCTCTCTGTTCTCTGTGATGCT	4833
		AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC ATTTCTTCTCTTGGACTAGGTGACCTGCCTGTTTGTTGGTTCTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	4834
		GTCACCTAGTCCAAGAG	4835
		CTCTTGGACTAGGTGAC	4836
15	Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAAACAAACAGG CAGGTCACCTACTCCTAGAGAAGAAATGGTTTGTTCAAGAAAGCAC ACGAGCTCTCTGTTCTCTGTGATGCTAAAG	4837
		CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA ACCATTTCTTCTCTAGGAGTAGGTGACCTGCCTGTTTGTTGGTTC TCTATCCTCTTAATCTGGATCTTCCCTCG	4838
		CCTACTCCTAGAGAAGA	4839
		TCTTCTCTAGGAGTAGG	4840
20	Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAAACAAACAGGCAG GTCACCTACTCCAAGTGAAGAAATGGTTTGTTCAAGAAAGCACACG AGCTCTCTGTTCTCTGTGATGCTAAAGTTT	4841
		AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA CAAACCATTTCTTCACTTGGAGTAGGTGACCTGCCTGTTTGTTGG TTCTCTATCCTCTTAATCTGGATCTTCCC	4842
		ACTCCAAGTGAAGAAAT	4843
		ATTTCTTCACTTGGAGT	4844
25	Male-sterile AP3 <i>Brassica napus</i> Arg25Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAAACAAACAGGCAGGTC ACCTACTCCAAGAGATGAAATGGTTTGTTCAAGAAAGCACACGAGC TCTCTGTTCTCTGTGATGCTAAAGTTTCCA	4845
		TGGAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT GAACAAACCATTTCACTCTTGGAGTAGGTGACCTGCCTGTTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	4846
		CCAAGAGATGAAATGGT	4847
		ACCATTTCACTCTTGG	4848

5	Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGT AGTGGTTCGATGGCTT <u>G</u> AGGGGAAGATCCAGATTAAGAGGATAGAG AACCAACAAACAGGCAGGTCACCTACTCCA	4849
		TGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAAT CTGGATCTTCCCTC <u>A</u> AGCCATCGAACCCTACCCTACTGCTCTTG TTTTCTTCTTCCAGCTTTCCTTTCTCTCC	4850
		CGATGGCTT <u>G</u> AGGGGAAG	4851
		CTTCCCTC <u>A</u> AGCCATCG	4852
10	Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGT <u>T</u> AGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTCACCTACTCCAAGAGAA	4853
		TTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCT CTTAATCTGGATCT <u>A</u> CCCTCGAGCCATCGAACCCTACCCTACTG CTCTTGTTTTCTTCTTCCAGCTTTCCTTT	4854
		CTCGAGGGT <u>T</u> AGATCCAG	4855
		CTGGATCT <u>A</u> CCCTCGAG	4856
15	Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGGAAGATCT <u>T</u> AGATTAAGAGGATAGAGAACCAAACAAC AGGCAGGTCACCTACTCCAAGAGAAGAAATG	4857
		CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTC TATCCTCTTAATCT <u>A</u> GATCTTCCCTCGAGCCATCGAACCCTACCA CTACTGCTCTTGTTTTCTTCTTCCAGCTT	4858
		GGAAGATCT <u>T</u> AGATTAAG	4859
		CTTAATCT <u>A</u> GATCTTCC	4860
20	Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATT <u>T</u> AGAGGATAGAGAACCAAACAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGTTTTGT	4861
		ACAAACCATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTG GTTCTCTATCCTCT <u>A</u> AATCTGGATCTTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTTGTTTTCTTCTTC	4862
		TCCAGATT <u>T</u> AGAGGATA	4863
		TATCCTCT <u>A</u> AATCTGGA	4864
25	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG	TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAAC TATGGCTCGTGGGT <u>T</u> AGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACTTATTCTAAGAGAA	4865
		TTCTCTTAGAATAAGTGACTTGCTGTTTGTTTGGTTCTCTATTCTC TTGATCTGGATCT <u>A</u> CCCACGAGCCATAGTTTTTTTTCTTTTTGCTC AAAGTTTGAGATCTTAAGAATTACTGA	4866
		CTCGTGGGT <u>T</u> AGATCCAG	4867
		CTGGATCT <u>A</u> CCCACGAG	4868

5	Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGC	4869
		TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAGA	
		CAAGTCACTTATTCTAAGAGAAGAAATG	
		CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGGTTCTCT	4870
		ATTCTCTTGATCTAGATCTTCCCACGAGCCATAGTTTTTTTTCTTT	
10	Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG	TTGCTCAAAGTTTGAGATCTTAAGAAT	
		GGAAGATCTAGATCAAG	4871
		CTTGATCTAGATCTTCC	4872
		AAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTG	4873
		GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAGT	
15	Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA	CACTTATTCTAAGAGAAGAAATGGACTTTT	
		AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGGT	4874
		TTCTCTATTCTCTAGATCTGGATCTTCCCACGAGCCATAGTTTTTT	
		TTCTTTTTGCTCAAAGTTTGAGATCTT	
		TCCAGATCTAGAGAATA	4875
20	Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	TATTCTCTAGATCTGGA	4876
		ATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTGGGA	4877
		AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCAC	
		TTATTCTAAGAGAAGAAATGGACTTTTCA	
		TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGT	4878
25	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	TGGTTCTCTATTCACTTGATCTGGATCTTCCCACGAGCCATAGTTT	
		TTTTTCTTTTTGCTCAAAGTTTGAGAT	
		AGATCAAGTGAATAGAG	4879
		CTCTATTCACTTGATCT	4880
		GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA	4881
	Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG	CAGACAAGTAACTTAGTCAAAACGAAGGGATGGTCTTTCAAGAAG	
		GCCAATGAGCTCACTGTTCTTTGTGATGCT	
		AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA	4882
		TCCCTTCGTTTTGACTAAGTTACTTGTCTGTTGTTGTTCTCTAT	
		TCTCTTGATCTGGATCTTTCCTCGAGCC	
	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	GTAACCTAGTCAAAACG	4883
		CGTTTTGACTAAGTTAC	4884
		CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA	4885
		GACAAGTAACTTACTGAAAACGAAGGGATGGTCTTTCAAGAAGGC	
		CAATGAGCTCACTGTTCTTTGTGATGCTAA	
	Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC	4886
		CATCCCTTCGTTTTCAGTAAGTTACTTGTCTGTTGTTGTTCTCT	
		ATTCTCTTGATCTGGATCTTTCCTCGAG	
		AACTTACTGAAAACGAA	4887
		TTCGTTTTCAGTAAGTT	4888

5	Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACTTACTCATAACGAAGGGATGGTCTTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTTGTGATGCTAAGG	4889
		CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG ACCATCCCTTCGTTATGAGTAAGTTACTTGTCTGTTTCGTTGTGTTCT CTATTCTCTTGATCTGGATCTTTCCTCG	4890
		CTTACTCATAACGAAGG	4891
		CCTTCGTTATGAGTAAG	4892
10	Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTTACTCAAAATGAAGGGATGGTCTTTTCAAGAAGGCCAATG AGCTCACTGTTCTTTGTGATGCTAAGGTTT	4893
		AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA AAGACCATCCCTTCAATTTTGAAGTAAGTTACTTGTCTGTTTCGTTGTGT TCTCTATTCTCTTGATCTGGATCTTTCC	4894
		ACTCAAAATGAAGGGAT	4895
		ATCCCTTCAATTTGAGT	4896
15	Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACTTACAGTTCTTTGTGATGCT	4897
		AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA TTTCTTCTCTTTGACTAAGTCACTTGCCTATTTGTTTGGTTTTCTATT TTCTTGATCTGGATCTTACCACGAGCC	4898
		GTGACTTAGTCAAAGAG	4899
		CTCTTTGACTAAGTCAC	4900
20	Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGCT AATGAACTTACAGTTCTTTGTGATGCTAA	4901
		TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC CATTCTTCTCTTTCAATAAGTCACTTGCCTATTTGTTTGGTTTTCTA TTTTCTTGATCTGGATCTTACCACGAG	4902
		GACTTATTGAAAGAGAA	4903
		TTCTCTTTCAATAAGTC	4904
25	Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGC AAGTGACTTATTCATAGAGAAGAAATGGGCTATTCAAGAAGGCTAA TGAAGTTACAGTTCTTTGTGATGCTAAG	4905
		CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGC CCATTTCTTCTCTATGAATAAGTCACTTGCCTATTTGTTTGGTTTTCT TATTTCTTGATCTGGATCTTACCACG	4906
		CTTATTCATAGAGAAGA	4907
		TCTTCTCTATGAATAAG	4908

5	Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAAG TGACTTATTCAAAGTGAAGAAATGGGCTATTCAAGAAGGCTAATGA ACTTACAGTTCTTTGTGATGCTAAAGTTT	4909
		AACTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAAT AGCCCATTTCTTCACTTTGAATAAGTCACCTTGCCTATTTGTTTGGTT TTCTATTTTCTTGATCTGGATCTTACC	4910
		ATTCAAAGTGAAGAAAT	4911
		ATTTCTTCACTTTGAAT	4912
10	Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA	GCTAATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTAT GATTTCTAGTACTTGAAAACCTTCATGAGTTTATAAGTCCCTCTATCA CGACCAAACAATTGTTTCGATCTGTACC	4913
		GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTTCAAGTACTAGAAATCATAACAATTGAACTTTAG CATCACAAAGAACAGTAAGTTCATTAGC	4914
		CTAGTACTTGAAAACCTT	4915
		AAGTTTTCAAGTACTAG	4916
15	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA	AATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGAT TTCTAGTACTGGATAACTTCATGAGTTTATAAGTCCCTCTATCACGA CCAAACAATTGTTTCGATCTGTACCAGA	4917
		TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTAT AACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAACTT TAGCATCACAAAGAACAGTAAGTTCATT	4918
		GTACTGGATAACTTCAT	4919
		ATGAAGTTATCCAGTAC	4920
20	Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTAC TGGAACCTTCATTAGTTTATAAGTCCCTCTATCACGACCAAACAAT TGTTTCGATCTGTACCAGAAGACTATTG	4921
		CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGA GGGACTTATAAACTAATGAAGTTTTCCAGTACTAGAAATCATAACAA TTGAACTTTAGCATCACAAAGAACAGT	4922
		AACTTCATTAGTTTATA	4923
		TATAAACTAATGAAGTT	4924
25	Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA	ATTGTTATGATTTCTAGTACTGGAAAACCTTCATGAGTTTATAAGTCC CTCTATCACGACCTAACAATTGTTTCGATCTGTACCAGAAGACTATT GGAGTTGATATTTGGACTACTCACTATG	4925
		CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAG ATCGAACAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA AGTTTTCCAGTACTAGAAATCATAACAAT	4926
		TCACGACCTAACAATTG	4927
		CAATTGTTAGGTCGTGA	4928

5	Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG	GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTAGTCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCCTGCTCTGCGACGCC	4929
		GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC CCGACCGGCGCTTGGACTAGGTACCTGCCTGTTGGTGGCGTTC TCGATCCGCTTTATCTCAATCTTCCCCCGCCCC	4930
		GTGACCTAGTCCAAGCG	4931
		CGCTTGGACTAGGTAC	4932
10	Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG	CGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCCTAGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCCTGCTCTGCGACGCCCAGG	4933
		CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG ATCCCCGACCGGCGCTAGGAGTAGGTACCTGCCTGTTGGTGGC GTTCTCGATCCGCTTTATCTCAATCTTCCCCCG	4934
		CCTACTCCTAGCGCCGG	4935
		CCGGCGCTAGGAGTAGG	4936
15	Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGTAGGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCGACGCCCAGGTGCGCCATCAT	4937
		ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTTCATGATCCCCTACCGGCGCTTGGAGTAGGTACCTGCCT GTTGGTGGCGTTCTCGATCCGCTTTATCTCAA	4938
		GCGCCGGTAGGGGATCA	4939
		TGATCCCCTACCGGCGC	4940
20	Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATGTAGAAGGCGCGGGAGCTCACCCTGCTCT GCGACGCCCAGGTGCGCCATCATCATGTTCTCCT	4941
		AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTTCTACATGATCCCCGACCGGCGCTTGGAGTA GGTCACTGCCTGTTGGTGGCGTTCTCGATCCG	4942
		GGATCATGTAGAAGGCG	4943
		CGCCTTCTACATGATCC	4944
25	Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTAGTCCAAGCGCCGGACGGGGATCATGAAG AAGGCACGCGAGCTCACCCTGCTCTGCGACGCC	4945
		GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCCTTCTTCATGATCC CCGTCCGGCGCTTGGACTAGGTACCTGGCGGTTGGTGGCGTTC TCGATCCGCTTGATCTCGATCTTGCCGCGCCCC	4946
		GTGACCTAGTCCAAGCG	4947
		CGCTTGGACTAGGTAC	4948

5	Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAAGG CACGCGAGCTCACCGTGCTCTGCCACGCCCAGG	4949
		CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG ATCCCCGTCCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	4950
		CCTACTCCTAGCGCCGG	4951
		CCGGCGCTAGGAGTAGG	4952
10	Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACGCGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	4953
		AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCGCGTGCCCTTCTACATGATCCCCGTCCGGCGCTTGGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	4954
		GGATCATGTAGAAGGCA	4955
		TGCCTTCTACATGATCC	4956
15	Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG	ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCG ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	4957
		TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCCTACTTCATGATCCCCGTCCGGCGCTTGA GTAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	4958
		TCATGAAGTAGGCACGC	4959
		GCGTGCCTACTTCATGA	4960
20	Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	4961
		GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTGCCTTCTCGATCC GCTTGATCTCGATCTAGCCCCTCCCCATGGCCGCCCCCTGCAGC AGCTATCTCTCTCGCCGGACAATGCAGCTAGC	4962
		GGAGGGGCTAGATCGAG	4963
		CTCGATCTAGCCCCTCC	4964
25	Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCA ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	4965
		CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTGCCTTCT CGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCTCGCCGGACAATGCA	4966
		GCAAGATCTAGATCAAG	4967
		CTTGATCTAGATCTTGC	4968

5	Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	4969
		TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTC GCGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCC GCCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	4970
		TCGAGATCTAGCGGATC	4971
		GATCCGCTAGATCTCGA	4972
10	Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	4973
		CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCC CCATGGCCGCCCCCTGCAGCAGCTATCTCTC	4974
		AGCGGATCTAGAACGCG	4975
		CGCGTTCTAGATCCGCT	4976

Table 15
Oligonucleotides to produce male-sterile plants

15	Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
20	Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	4977
		TTCGATCTTTCCTCTCCCAGATTTCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAAA ACGTTTAGGGCAAATTTGATTAGTACAGA	4978
		ACGGCGTAGCAATCGGA	4979
		TCCGATTGCTACGCCGT	4980
25	Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCTCTCCCT TGAGGAAATCTGGGAGAGGAAAGATCGAAA	4981
		TTTCGATCTTTCCTCTCCCAGATTTCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAAA AACGTTTAGGGCAAATTTGATTAGTACAG	4982
		CGGCGTACTAATCGGAG	4983
		CTCCGATTAGTACGCCG	4984

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG	ACTAATCAAATTTTGGCCTAAACGTTTTGGCTTTGGAGCAGCAAT CACGGCGTACCAATAGGAGCTAGGAGGAGATTCTCTCCCTTGA GGAAATCTGGGAGAGGAAAGATCGAAATCAA	4985
	TTGATTTGATCTTTCTCTCCCAGATTTCTCAAGGGAGAGGAAT CTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGC CAAAAACGTTTAGGGCAAAATTTGATTAGT	4986
	GTACCAATAGGAGCTAG	4987
	CTAGCTCCTATTGGTAC	4988
10 Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG	TAATCAAATTTTGGCCTAAACGTTTTGGCTTTGGAGCAGCAATCA CGGCGTACCAATCGTAGCTAGGAGGAGATTCTCTCCCTTGAGGA AATCTGGGAGAGGAAAGATCGAAATCAAAC	4989
	GTTTGATTTGATCTTTCTCTCCCAGATTTCTCAAGGGAGAGGA ATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAA GCCAAAACGTTTAGGGCAAAATTTGATTA	4990
	ACCAATCGTAGCTAGGA	4991
	TCCTAGCTACGATTGGT	4992
15 Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCA CAGAAGCAATGGATTAAGGTGGGAGTAGTCACGATGCAGAGAGTA GCAAGAAGATAGGTAGAGGGAAGATAGAGA	4993
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTG ACTACTCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAAT GAATAAACCACCGAAAAGAAGTGGGAGAG	4994
	CAATGGATTAAGGTGGG	4995
	CCCACCTTAATCCATTG	4996
20 Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGG AGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAAG ATAGAGATAAAGAGGATAGAGAACACAACAA	4997
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATC TTCTTGCTACTCTATGCATCGTGACTACTCCACCTTCATCCATTG CTTCTGTGATATCGTCACCAAATGAATA	4998
	ACGATGCATAGAGTAGC	4999
	GCTACTCTATGCATCGT	5000
25 Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCA CGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGAT AAAGAGGATAGAGAACACAACAAATCGTCAAG	5001
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCT CTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCACCTT CATCCATTGCTTCTGTGATATCGTCACC	5002
	AGAGTAGCTAGAAGATA	5003
	TATCTTCTAGCTACTCT	5004

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGAT GCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAGATAGAGATAAAG AGGATAGAGAACACAACAAATCGTCAAGTAA	5005
	T TACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC CCTCTACCTATCTACTTGCTACTCTCTGCATCGTGACTACTCCAC CTTCATCCATTGCTTCTGTGATATCGTC	5006
	GTAGCAAGTAGATAGGT	5007
	ACCTATCTACTTGCTAC	5008
10 Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA	CAACCAAAAACTTAAAAATCTTCTCTTTCTTTCTTACAAGGTGA AGTAATGGACTTCTAAAGTGATCTAACCAGAGAGATCTCACCACAA AGGAACTAGGAAGGGGGAAAATTGAGA	5009
	TCTCAATTTTCCCCCTTCTAGTTTCTTTGTGGTGAGATCTCTCT GGTTAGATCACTTTAGAAGTCCATTACTTCACCTTGTAAGGAAAGG AAAGAGAAGATTTTTAAGTTTTTGGTTG	5010
	TGGACTTCTAAAGTGAT	5011
	ATCACTTTAGAAGTCCA	5012
15 Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA	AAAATCTTCTCTTTCTTTCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACCAGAGATCTCACCACAAAGGAACTAGGAA GGGGGAAAATTGAGATCAAAGGATCGAAA	5013
	TTTCGATCCTTTTGATCTCAATTTTCCCCCTTCTAGTTTCTTTGT GGTGAGATCTCTCAGGTTAGATCACTTTGGAAGTCCATTACTTCAC CTTGTAAGGAAAGGAAAGAGAAGATTTT	5014
	ATCTAACCAGAGATC	5015
	GATCTCTCAGGTTAGAT	5016
20 Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG	ATCTTCTCTTTCTTTCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCAGATAGATCTCACCACAAAGGAACTAGGAAGGG GGAAAATTGAGATCAAAGGATCGAAAACA	5017
	TGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCTAGTTTCTTT TGTGGTGAGATCTATCTGGTTAGATCACTTTGGAAGTCCATTACTT CACCTTGTAAGGAAAGGAAAGAGAAGAT	5018
	TAACCAGATAGATCTCA	5019
	TGAGATCTATCTGGTTA	5020
25 Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA	CTTTCCTTTCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCTGACCACAAAGGAACTAGGAAGGGGGAAAAT TGAGATCAAAGGATCGAAAACACGACGAA	5021
	TTCGTCGTGTTTTGATCCTTTTGATCTCAATTTTCCCCCTTCTA GTTTCTTTGTGGTCAGATCTCTCTGGTTAGATCACTTTGGAAGTC CATTACTTCACCTTGTAAGGAAAGGAAAG	5022
	AGAGATCTGACCACAAA	5023

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TTTGTGGT <u>C</u> AGATCTCT	5024
5 Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA	GTACTCTCTATTTTCATCTTCCAACCCTTTCTTTCTTACCAGGTGA AAGTATGGACTTCTAAAGTGATCTAACAAGAGAGATCTCTCCACAA AGGAACTGGGAAGAGGAAAGATTGAGA	5025
	TCTCAATCTTTCTCTTCCCAGTTTCTTTGTGGAGAGATCTCTCT TGTTAGATCACTTTAAGAGTCCATACTTTACCTGGTAAGGAAAGA AAGGGTTGGAAGATGAAATAGAGAGTAC	5026
	TGGACTTCTAAAGTGAT	5027
	ATCACTTTAAGAGTCCA	5028
10 Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA	ATCTTCCAACCCTTTCTTTCTTACCAGGTGAAAGTATGGACTTCC AAAGTGATCTAACAATGAGAGATCTCTCCACAAAGGAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA	5029
	TTTCGATCCGTTTGATCTCAATCTTTCTCTTCCCAGTTTCTTTGT GGAGAGATCTCTCATGTTAGATCACTTTGGAAGTCCATACTTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT	5030
	ATCTAACATGAGAGATC	5031
	GATCTCTCATGTTAGAT	5032
15 Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG	TTCCAACCCTTTCTTTCTTACCAGGTGAAAGTATGGACTTCCAAA GTGATCTAACAAGATAGATCTCTCCACAAAGGAACTGGGAAGAG GAAAGATTGAGATCAAACGGATCGAAAACA	5033
	TGTTTTCGATCCGTTTGATCTCAATCTTTCTCTTCCCAGTTTCTTT TGTGGAGAGATCTATCTTGTTAGATCACTTTGGAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGAA	5034
	TAACAAGATAGATCTCT	5035
	AGAGATCTATCTTGTTA	5036
20 Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAA GAGAGATCTCTCCATAAAGGAACTGGGAAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC	5037
	GACGATTCGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCTCT TCCCAGTTTCTTTATGGAGAGATCTCTTGTAGATCACTTTGG AAGTCCATACTTTACCTGGTAAGGAAAG	5038
	TCTCTCCATAAAGGAAA	5039
	TTTCCTTTATGGAGAGA	5040
25 Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAA AGAAGATTGGGAAGGTGAAAGATCGAGATCAAGCGGATCGAAAAC ACCACCAATCGTCAAGTCACCTTCTGCAAAA	5041
	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCCGCT TGATCTCGATCTTTCACCTTCCCAATCTTCTTTGGGCATCAGCGTC CAGGACCGTGTGGGTTTGTTCATAGGC	5042
	TGGGAAGGTGAAAGATC	5043
	GATCTTTCACCTTCCCA	5044

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGA AGATTGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAAGGC	5045
	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCTATCCCCTTCCCAATCTTCTTTGGGCATCAGC GTCCAGGACCGTGTTGGGTTTGTTCATA	5046
	GAAGGGGATAGATCGAG	5047
	CTCGATCTATCCCCTTC	5048
10 Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAAT CGTCAAGTCACCTTCTGCAAAAGGCGCAATG	5049
	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTC CGATCCGCTTGATCTAGATCTTCCCCTTCCCAATCTTCTTTGGGC ATCAGCGTCCAGGACCGTGTTGGGTTTGT	5050
	GAAAGATCTAGATCAAG	5051
	CTTGATCTAGATCTTTC	5052
15 Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	5053
	GCAAAACATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTTCGATCCGCTAGATCTCGATCTTCCCCTTCCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTTGGG	5054
	TCGAGATCTAGCGGATC	5055
	GATCCGCTAGATCTCGA	5056
20 Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA	CAATTGCCTGTTTTATTTTTTTCTTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAAATCGACCGAGGTATCGCCCGAGAGGAAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	5057
	TCCGTTTGATCTCGATCTTTCCTCTCCCGATTTCTCTCGGGCGA TACCTCGGTGATTAAATCGCTTAGAGACGCCATTTCTACTTAGTCA AAAAGAAAAAAATAAAAAACAGGCAATTG	5058
	TAAGCGATTAAATCGACC	5059
	GGTCGATTAAATCGCTTA	5060
25 Male-sterile far <i>Antirrhinum majus</i> Glu10Term GAG-TAG	GTTTTATTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	5061
	TGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTCTCT CTCGGGCGATACCTAGGTGATTGATCGCTTAGAGACGCCATTTCT TACTTAGTCAAAAAGAAAAAAATAAAAAAC	5062
	AATCGACCTAGGTATCG	5063
	CGATACCTAGGTGATT	5064

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA CCGAGGTATCGCCCTAGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAAACAAATCAAC	5065
	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC CCGATTTTCCTCTAGGGCGATACCTCGGTGATTGATCGCTTAGA GACGCCATTTCTACTTAGTCAAAAAGAAA	5066
	TATCGCCCTAGAGGAAA	5067
	TTTCCTCTAGGGCGATA	5068
10 Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG GTATCGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAAACAAATCAACAGGTGA	5069
	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT CCTCTCCCATTACCTCTCGGGCGATACCTCGGTGATTGATCG CTTAGAGACGCCATTTCTACTTAGTCAAA	5070
	CCGAGAGGTAAATCGGG	5071
	CCCGATTTACCTCTCGG	5072
15 Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGTAGCAATAAAGGGGATGTTCCAGAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	5073
	TTCCTCTGAGGCGAGTCTGACATCTTCTTCTTGATTCTGGAACA TCCCCTTTATTTGCTACTTACCCTTTCTTCTTCTTCTTAAATCATTCT GTGAGTGGTGACTGATAATGCTTGGACA	5074
	GGGTAAGTAGCAATAA	5075
	TTATTTGCTACTTACCC	5076
20 Male-sterile AG <i>Cucumis sativus</i> Gln22Term CAA-TAA	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAG GAAAGGGTAAGTTGTAAATAAAGGGGATGTTCCAGAATCAAGAAG AGAAGATGTCAGACTCGCCTCAGAGGAAGA	5077
	TCTTCCTCTGAGGCGAGTCTGACATCTTCTTCTTGATTCTGGAA CATCCCCTTTATTTCAAACTTACCCTTTCTTCTTCTTCTTAAATCATTCT TTGTGAGTGGTGACTGATAATGCTTGGAA	5078
	GTAAGTTGTAAATAAAG	5079
	CTTTATTTCAAACTTAC	5080
25 Male-sterile AG <i>Cucumis sativus</i> Lys24Term AAG-TAG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATATAGGGGATGTTCCAGAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAGATGGGAA	5081
	TTCCCATCTTCTCTGAGGCGAGTCTGACATCTTCTTCTTGATT CTGGAACATCCCCTATATTTGCAACTTACCCTTTCTTCTTCTTCTTAAATCATTCT ATCATTCTTGTGAGTGGTGACTGATAATG	5082
	TGCAAATATAGGGGATG	5083
	CATCCCCTATATTTGCA	5084

[illegible]

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTGACCCCTGACTTCGGCGG	5105
	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTCAGATGTGCATGCTCTTGTTCCATCACACA GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	5106
	TGCACATCTGAGAAGAG	5107
	CTCTTCTCAGATGTGCA	5108
10 Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTGACCCCTGACTTCGGCGGGG	5109
	GCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTTATCGGATGTGCATGCTCTTGTTCCATCA CACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	5110
	ACATCCGATAAGAGGAG	5111
	CTCCTCTTATCGGATGT	5112
15 Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAAATAGGAGGCTACACCATCCACAGTAACAGGCA TCATGTGACCCCTGACTTCGGCGGGGCGAGC	5113
	GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCCTATTCTCGGATGTGCATGCTCTTGTTCTTA TCACACAGATTTTGAGGTCTGAAGGAGAAAAG	5114
	TCCGAGAAATAGGAGGCT	5115
	AGCCTCCTATTCTCGGA	5116
20 Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATGC ACATCCGAGAAAGAGTAGGCTACACCATCCACAGTAACAGGCATCA TGTCGACCCCTGACTTCGGCGGGGCGAGCAGA	5117
	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCTACTCTTCTCGGATGTGCATGCTCTTGTTCT CTATCACACAGATTTTGAGGTCTGAAGGAGAA	5118
	GAGAAGAGTAGGCTACA	5119
	TGTAGCCTACTCTTCTC	5120
25 Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG	GCTGGGTGAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC GAGAAGATGGGGAGGGGGTAGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	5121
	GGCGCTTGAGAAGGTACCTGCCGGTTCGTGTTCTCGATC CGCTTTATCTCGATCTACCCCTCCCATCTTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	5122
	GGAGGGGGTAGATCGAG	5123
	CTCGATCTACCCCTCC	5124

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGA TGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACG AACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	5125
	CATTGCGGCGCTTGCAGAAGGTCACCTGCCGTTTCGTCTGTTC TCGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTG CTCCCCGCCGCCACCGCCGCCGACGATCCTGA	5126
	GGAAGATCTAGATAAAG	5127
	CTTTATCTAGATCTTCC	5128
10 Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG	TCGTGCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGG AGGGGGAAGATCGAGATATAGCGGATCGAGAACACGACGAACCG GCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	5129
	GGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGTTTCGTCT GTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCT CGCTGCTCCCCGCCGCCACCGCCGCCGACGA	5130
	TCGAGATATAGCGGATC	5131
	GATCCGCTATATCTCGA	5132
15 Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	5133
	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGC CGGTTCTGTCGTGTTCTAGATCCGCTTTATCTCGATCTTCCCCCTC CCCATCTTCTCGCTGCTCCCCGCCGCCACCGC	5134
	AGCGGATCTAGAACACG	5135
	CGTGTTCTAGATCCGCT	5136

Table 16
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
20 Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAAT AGACAAGTTACATAGTCAAAGAGAAGAAATGGTATCATCAAAAAG CCAAAGAAATTACTGTTCTTTGCGATGCT	5137
	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTATGATGATACCAT TTCTTCTCTTTGACTATGTAACCTGTCTATTGCTTGAGTTCTCTATTC TTTTATTCTATTTCCCTCTTCCC	5138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GTTACATAGTCAAAGAG	5139
	CTCTTTGACTATGTAAC	5140
Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA	GAAGAGGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAG ACAAGTTACATATTGAAAGAGAAGAAATGGTATCATCAAAAAGCC AAAGAAATTACTGTTCTTTGCGATGCTCA	5141
	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACC ATTTCTTCTCTTTCAATATGTAACCTGTCTATTGCTTGAGTTCTCTAT TCTTTTATTTCTATTTTCCCTCTTC	5142
	TACATATTGAAAGAGAA	5143
	TTCTCTTTCAATATGTA	5144
Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG	AGAGGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATTCATAGAGAAGAAATGGTATCATCAAAAAGCCAAA GAAATTACTGTTCTTTGCGATGCTCAAG	5145
	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATA CCATTTCTTCTCTATGAATATGTAACCTGTCTATTGCTTGAGTTCTC TATTTCTTTTATTTCTATTTTCCCTCT	5146
	CATATTCATAGAGAAGA	5147
	TCTTCTCTATGAATATG	5148
Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATTCAAAGTGAAGAAATGGTATCATCAAAAAGCCAAAGAA ATTACTGTTCTTTGCGATGCTCAAGTTT	5149
	AACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATG ATACCATTTCTTCACTTTGAATATGTAACCTGTCTATTGCTTGAGTT CTCTATTCTTTTATTTCTATTTTCCC	5150
	ATTCAAAGTGAAGAAAT	5151
	ATTTCTTCACTTTGAAT	5152
Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCTAGTCCAAGAGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTTCTATGTGATGCT	5153
	AGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCA TTCCTCCTCTTGGACTAGGTACCTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTTCCCACGTCCC	5154
	GTGACCTAGTCCAAGAG	5155
	CTCTTGGACTAGGTAC	5156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Male-sterile PI <i>Malus domestica</i> Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG	5157
	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC CCATTCCTCCTCTAGGAGTAGGTACCTGCCTGTTACTTGAGTTCT CAATCCTCTTGATCTCAACCTTCCCACG	5158
	CCTACTCCTAGAGGAGG	5159
	CCTCCTCTAGGAGTAGG	5160
10 Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAAGGCAAAGGAGATCACTGTTCTATGTG ATGCTAAAGTATCTCTTATCATTTATTCTA	5161
	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGATC TCCTTTGCCTTCTAGATAATCCCATTCCTCCTCTTGGAGTAGGTCA CCTGCCTGTTACTTGAGTTCTCAATCCT	5162
	GGATTATCTAGAAGGCA	5163
	TGCCTTCTAGATAATCC	5164
15 Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTTATTCTAGCT	5165
	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT GATCTCCTTTGCCTACTTGATAATCCCATTCCTCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT	5166
	TTATCAAGTAGGCAAAG	5167
	CTTTGCCTACTTGATAA	5168
20 Male-sterile globosa <i>Antirrhinum majus</i> Gly2Term GGA-TGA	CATTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	5169
	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTGATCTCA ATTTTTCCTCTTCAATTTTTTTGTTTTTCTCTCTTGTGTTTTG TTTGCAGATAACTATTGTAAAAATG	5170
	AAAAAATGTGAAGAGGA	5171
	TCCTCTTCAATTTTTT	5172
25 Male-sterile globosa <i>Antirrhinum majus</i> Arg3Term AGA-TGA	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAA CAAAAAAATGGGATGAGGAAAAATTGAGATCAAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	5173
	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTGATC TCAATTTTCTCTCATCCCATTTTTTTGTTTTTCTCTCTTGT TTTGTGTTGCAGATAACTATTGTAAAA	5174

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	AAATGGGAT <u>T</u> GAGGAAAA	5175
	TTTTCTC <u>A</u> TCCCATT	5176
Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAA AAAAATGGGAAGAT <u>T</u> GAAAAATTGAGATCAAAAGAATTGAGAACTCA AGCAACAGGCAGGTTACTTACTCAAAGA	5177
	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTG ATCTCAATTTTT <u>C</u> ATCTTCCCATTTTTTTGTTTTGTTTTCTCTCTT GTTTTGTTTGCAGATAACTATTGTA	5178
	TGGGAAGAT <u>T</u> GAAAAATT	5179
	AATTTTT <u>C</u> ATCTTCCCA	5180
Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA AATGGGAAGAGGAT <u>A</u> AATTGAGATCAAAAGAATTGAGAACTCAAGC AACAGGCAGGTTACTTACTCAAAGAGAA	5181
	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATTT <u>A</u> TCCTCTTCCCATTTTTTTGTTTTGTTTTCTCT CTTGTTTTGTTTGCAGATAACTATT	5182
	GAAGAGGAT <u>A</u> AATTGAG	5183
	CTCAATTT <u>A</u> TCCTCTTC	5184
Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGC AGTATGGGGCGCGGCT <u>T</u> AGATCAAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5185
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTTGATCT <u>A</u> GCCGCGCCCCATACTGCGTTCTCCACTCC CAAACAGATCCAAGGGCAGCAAGAGCTCAGC	5186
	GGCGCGGCT <u>T</u> AGATCAAG	5187
	CTTGATCT <u>A</u> GCCGCGCC	5188
Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATC <u>T</u> AGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5189
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCT <u>A</u> GATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	5190
	GCAAGATC <u>T</u> AGATCAAG	5191
	CTTGATCT <u>A</u> GATCTTGC	5192

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5193
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	5194
	GCAAGATCTAGATCAAG	5195
	CTTGATCTAGATCTTGC	5196
10 Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGATCTAGA ACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGACTGGTCAAGAAGG	5197
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTTGATCTTGCCGCGC CCCATACTGCGTTCTCCACTCCCAAACAGATC	5198
	AGAGGATCTAGA ACTCT	5199
	AGAGTTCTAGATCCTCT	5200
15 Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGGCTAGATCGAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	5201
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGATCTAGCCGCGCCCCATACTCCGTTCTCCACTCC CTAACAGATTCAAGGGCAGCAAGAGCTCAGC	5202
	GGCGCGGCTAGATCGAG	5203
	CTCGATCTAGCCGCGCC	5204
20 Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	5205
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	5206
	GCAAGATCTAGATCAAG	5207
	CTTGATCTAGATCTTGC	5208
25 Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCA GGTGACCTTCTCCAAGCGCCGGGCCGACTGG	5209
	CCAGTCCGGCCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTA GAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	5210

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCGAGATCTAGAGGATC	5211
	GATCCTCTAGATCTCGA	5212
Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	5213
	CCTTCTTGACCAGTCCGGCCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTCGATCTTGCCGCGC CCCATACTCCGTTCTCCACTCCCTAACAGATT	5214
	AGAGGATCTAGAACTCT	5215
	AGAGTTCTAGATCCTCT	5216
Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	5217
	TGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCC TCTTGATCTCGATCTACCCGCGCCCCATCCCGCCTCCTCCTCCTC CTCCTCCTCCTCCAGCTAGCTTAGCAGCAA	5218
	GGCGCGGGTAGATCGAG	5219
	CTCGATCTACCCGCGCC	5220
Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGCGGGA TGGGGCGCGGGAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	5221
	CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTC TCGATCCTCTTGATCTAGATCTTCCGCGCCCCATCCCGCCTCCT CCTCCTCCTCCTCCTCCTCCTCCAGCTAGCTTAG	5222
	GGAAGATCTAGATCAAG	5223
	CTTGATCTAGATCTTCC	5224
Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC GCGGGAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	5225
	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTG GAGTTCTCGATCCTCTAGATCTCGATCTCCCGCGCCCCATCCCG CCTCCTCCTCCTCCTCCTCCTCCTCCTCCAGCTA	5226
	TCGAGATCTAGAGGATC	5227
	GATCCTCTAGATCTCGA	5228

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI <i>Oryza sativa</i> Glu12Term GAG-TAG	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAGA TCGAGATCAAGAGGATCTAGAACTCCACCAACCGCCAGGTGACCT TCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	5229
	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGC GGTTGGTGGAGTTCTAGATCCTCTTGATCTCGATCTTCCGCGCC CCATCCCGCCTCCTCCTCCTCCTCCTCCTC	5230
	AGAGGATCTAGAACTCC	5231
	GGAGTTCTAGATCCTCT	5232

Example 7**Engineering plants for abiotic stress tolerance**

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhanced flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 17
Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGT <u>GCT</u> AGAGATAAGGATTTGAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	5233
	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTA <u>GCA</u> CTGCTATCGGTCACAAGCATTGAGCAACC GTCACATCCAACTACCACACAAAAAGACG	5234
	ATAGCAGT <u>GCT</u> AGAGAT	5235
	ATCTCTA <u>GCA</u> CTGCTAT	5236
Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC	GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT <u>GCC</u> CAGAGACAAGGAGTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA	5237
	TCAAATCAAGCATGGACTTCACTGTCTCATTAAAGTTGCTTCCTGAA CTCCTTGTCTCTG <u>GCA</u> CTACTGTCAATCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	5238
	ACAGTAGT <u>GCC</u> CAGAGAC	5239
	GTCTCTG <u>GCA</u> CTACTGT	5240
Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT <u>GTC</u> CAGAGATAAGGATTTGAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	5241
	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGA <u>CA</u> CTGCTATCAGTCACCAGCATTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	5242
	ATAGCAGT <u>GTC</u> CAGAGAT	5243
	ATCTCTGA <u>CA</u> CTGCTAT	5244
Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGAT <u>GCT</u> GAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	5245
	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCA <u>GCA</u> TCACTGTCCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC	5246
	ACAGTGAT <u>GCT</u> GAGAAC	5247
	GTTCTCA <u>GCA</u> TCACTGT	5248

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT	GATATTTTGTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG TACTGACAATGATGCTAGAGACCAAGATTTAGAAAGCAACTTTC TGAAACTGTGAGATCACTTCTAGCACTAA	5249
	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA ATCTTGGTCTCTAGCATCATTGTGAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC	5250
	ACAATGATGCTAGAGAC	5251
	GTCTCTAGCATCATTGT	5252
10 Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT	GATACATTGTTTGTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGATGCTAGGGATCCAGAATTCAGGAAGCAACTTA CTGAAACTGTAGAATCACTATTGAATTTGA	5253
	TCAAATTC AATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT TCTGGATCCCTAGCATCATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAATGTATC	5254
	ATAATGATGCTAGGGAT	5255
	ATCCCTAGCATCATTAT	5256
15 Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGACGCCAGGAAGTCCAGAATTTAGAAAACAACTTA CTGAAACAGTCGATTCTTTATTATCTTATA	5257
	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT TCTGGACTTCTGGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC	5258
	ATAATGACGCCAGGAAGT	5259
	ACTTCTGGCGTCATTAT	5260
20 Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT	GATTCTTTGTTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGACGCTAGAGATCCAGATTTTAGGAGACAACCTCAA TGACACAGTAAATTCGTTGCTTTCTCTAA	5261
	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA ATCTGGATCTCTAGCGTCATTATCAGTCACCAGAAGCTGAGCTGA TGTCACATCCAAGTACTGAACAAAGAATC	5262
	ATAATGACGCTAGAGAT	5263
	ATCTCTAGCGTCATTAT	5264
25 Salt Tolerance P5CS <i>Vigna unguiculata</i> Phe162Ala TTT-GCT	GATACCATGTTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATTTGCTAGGGATGCTGGCTTCAGAAAACAACTTTC GGACACAGTGAACGCGTTATTAGATTTAA	5265
	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA GCCAGCATCCCTAGCAAATCCATCATTACAAGAAGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	5266
	ATGGATTTGCTAGGGAT	5267

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATCCCTAGCAAATCCAT	5268
5 Salt Tolerance P5CS <i>Mesembryanthemum crystallinum</i> Phe125Ala TTT-GCT	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGACGCTAGAGATCCAAGTTTTAGAACAACAACTA ACTGAAACAGTGTATCAGTTGTTGGATCTAA	5269
	TTAGATCCAACAACGATACACTGTTTCAGTTAGTTGTGTTCTAAAA CTTGGATCTCTAGCGTCGTTGTCCGTCACAAGCAGCTGAGCAGCA GTCAGATCCAACGACTAAACAAGGTGTC	5270
	ACAACGACGCTAGAGAT	5271
	ATCTCTAGCGTCGTTGT	5272
10 Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGATGCTAGGGATGAAGCTTTCCGAAATCAACTTA CTCAAACAGTGGATTCAATTGTTAGCTTTGA	5273
	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCCGAA AGCTTCATCCCTAGCATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	5274
	ATAATGATGCTAGGGAT	5275
	ATCCCTAGCATCATTAT	5276
15 Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGATGCTCGAGATAAGGATTTCCAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	5277
	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA AATCCTTATCTCGAGCATCGTTATCCGTCACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACAGCGTATC	5278
	ATAACGATGCTCGAGAT	5279
	ATCTCGAGCATCGTTAT	5280
20 Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCG TCTTCACAACAGTTGTCACGTTTGCAAACGCGGATTTGTCCCCAC GAATGAGAACATGATCATCTTTCGCAAAA	5281
	TTTTGCGAAAGATGATCATGTTCTCATTCTGTTGGGACAAATCCGCA GTTTGCAAACGTAACAACGTTGTGAAGACGGAGAAAGTGAGAGG TGAGATTTCTTTGGAACATAAGAACATCTCT	5282
	CAACAGTTGTCACGTTT	5283
	AAACGTGAACAACGTTG	5284
25 Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTTCGCAAAAACCTCTGGTCTCATCTG GCTCCTAATCCCTCTAGTACTGATGGGAAACACTTTGTTCCCTTGC TTCTTGGTTTTGCTCATATGGGGACTTTA	5285
	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGAACAAAGTG TTTCCCATCAGTACTAGAGGGATTAGGAGCCAGATGAGACCAGAG TTTTTGCGAAAGATGATCATGTTCTCATTCTG	5286

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTCTAGTACTGA	5287
	TCAGTACTAGAGGGATT	5288
5 Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGAGTTCGCGACACACCGGAGAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT	5289
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAACTCACCACCTTGAAACAACGATCCAACCAAC TTCTCGTACGAACCTATTCTTCTAGAGACT	5290
	AGTGGTGAGTTCGCGAC	5291
	GTCGCGAACTCACCACCT	5292
10 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTGTTGACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA	5293
	TTTTGCTGAAGATAATCATGTTTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGTCACACCGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT	5294
	CCACCGTGTTGACCTTT	5295
	AAAGGTCACACCGGTGG	5296
15 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG	CCAATGAAAACATGATTATCTTCAGCAAAAACCTCTGGCCTCCTCCT GATTCTCATCCCTCTGGCCCTTCTTGGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG	5297
	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCCAGAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTTCATTGG	5298
	CATCCCTCTGGCCCTTC	5299
	GAAGGGCCAGAGGGATG	5300
20 Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGAGCAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	5301
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTGCTCAGCAGCACTGAAACAGCGCGCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	5302
	GTGCGTGAGCAGCAGAC	5303
	GTCTGCTGCTCAGGCAC	5304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCAT TCTCGGTCACGGTCTCTCGTTTGCGAATGTGGGGCTCGTGCCG ACAAATGAGAACATGGCAATCTTCTCCAAGA	5305
	TCTTGGAGAAGATTGCCATGTTCTCATTTGTGCGGCACGAGCCCCA CATTGCGAAACGAGACGACCGTGACCGAGAATGAGAAGAGTGCA ATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	5306
	TCACGGTCTCTCGTTT	5307
	AAACGAGACGACCGTGA	5308
10 Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCC TCCTGTTTCATCGGCCCTGATTCTTGCAAGCAATACACTTTACCCTCT CTTCCTAAGGCTATTGATATGGTTCCTGGG	5309
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAATCAGGCCGATGAACAGGAGGAGGAGGCCCGG GTTCTTGGAGAAGATTGCCATGTTCTCATTTG	5310
	CATCGGCCCTGATTCTTG	5311
	CAAGAATCAGGCCGATG	5312
15 Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATT GTTTCATGGCAGTGACGCGCAAGGCACTCGGGGGAGAACTCCATCG ACTGCTCACTCATCGCCCTGCTGTTCTAGT	5313
	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCCCTTGCGCTCACTGCCATGAACAATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	5314
	GGCAGTGAGCGCAAGGC	5315
	GCCTTGCGCTCACTGCC	5316
20 Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCAC TATCAGTCACCGTTGTCTCCTGTGCGAATGCAGGACTCGTGCCCA CAAATGAGAACATGGTCATCTTCTCAAAGAA	5317
	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCT GCATTGCGACAGGAGACAACGGTGACTGATAGTGAGAAGAGCAC GATGTTGATCCCTTTCTTGTTCACTGGGGCAC	5318
	CACCGTTGTCTCCTGTG	5319
	CACAGGAGACAACGGTG	5320
25 Salt Tolerance HKT1 <i>Triticum aestivum</i> Gln270Leu CAG-CTG	CAAATGAGAACATGGTCATCTTCTCAAAGAATTCAGGCCTCTTGTT GCTGCTGAGTGGCCCTGATGCTCGCAGGCAATACATTGTTCCCTCT CTTCCTGAGGCTACTGGTGTGGTTCTGCG	5321
	CCCAGGAACCAACAGTAGCCTCAGGAAGAGAGGGAACAATGT ATTGCCTGCGAGCATCAGGCCACTCAGCAGCAACAAGAGGCCTG AATTCTTTGAGAAGATGACCATGTTCTCATTTG	5322
	GAGTGGCCCTGATGCTCG	5323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGAGCATC <u>A</u> GGCCACTC	5324
5 Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGA <u>G</u> TGCGAGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	5325
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCA <u>C</u> TACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	5326
	GGTGGTGA <u>G</u> TGCGAGGC	5327
	GCCTCGCA <u>C</u> TACCACC	5328
10 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA	TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCA ACCCGTCTTCTC <u>T</u> GAACAACTTTATCCGGCGATCTTACCGTTTAC CCGCTTTTAGCCCGGTGGGTCTCTCCA	5329
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAGTTTGTTC <u>A</u> GAGAAGACGGGTTGCCATAAAATTCAAA GATTTTGTTTTTGAAAACGAAAACAAAAAAA	5330
	GTCTTCTC <u>T</u> GAACAAAC	5331
	GTTTGTTC <u>A</u> GAGAAGAC	5332
15 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAA CAAACCTTTATCCGGT <u>G</u> ATCTTACCGTTTACCCGCTTTTAGCCCGGT GGGTCTCTCCACCGTGACTGCTTCCACCG	5333
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATC <u>A</u> CCGGATAAAGTTTGTCTGAGAAGACG GGTTGCCATAAAATTCAAAGATTTTGTTTTTGA	5334
	TTATCCGGT <u>G</u> ATCTTAC	5335
	GTAAGATC <u>A</u> CCGGATAA	5336
20 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTTA TCCGGCGATCTTA <u>G</u> CGTTTACCCGCTTTTAGCCCGGTGGGTCTC CCACCGTGACTGCTTCCACCGCCGTCGTC	5337
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACG <u>C</u> TAAGATCGCCGGATAAAGTTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTTT	5338
	CGATCTTA <u>G</u> CGTTTACC	5339
	GGTAAACG <u>C</u> TAAGATCG	5340

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTTATCCG GCGATCTTACCGTTAACCCTGCTTTAGCCCGGTGGGTCTCCAC CGTGACTGCTTCCACCGCCGTCGTCCCGGA	5341
	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA CCGGGCTAAAAGCGGGTTAACGGTAAGATCGCCGGATAAAGTTTG TTCGGAGAAGACGGGTTGCCATAAAATTCAAAG	5342
	TTACCGTTAACCCTGCTT	5343
	AAGCGGGTTAACGGTAA	5344
10 Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA	CCGGTGGGTCTCCACCGTGACTGCTTCCACCGCCGTCGTCC GGAGATTCTCTCTTTTGACAACAAGCACCGGAACCACTCTTCA CCACCCAAAACCCACCGAGCAATCTCACGATG	5345
	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTTGTCAAAAGGAGAGAATCTCCGGGACGACGGC GGTGAAGCAGTCACGGTGGGAGGACCCACCGG	5346
	TCTCCTTTTGACAACAA	5347
	TTGTTGTCAAAAGGAGA	5348
15 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTCA AACTATGAATTTCTGACAAGAGAAGTTTGTAAGGTCAGTGTTCCAG ATTTGTCTCATTGAATTCTAAGTCGTGA	5349
	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AACTTCTCTTGTCAGAAATTCATAGTTTGAGACTAATAAGATTCAA TACAAACAGAGATTTCACTGCTTCATGT	5350
	TGAATTTCTGACAAGAG	5351
	CTCTTGTCAGAAATTCA	5352
20 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTCAAAC TATGAATTTCCGATAAGAGAAGTTTGTAAGGTCAGTGTTCCAGATT TGTCTCATTGAATTCTAAGTCGTGAAGC	5353
	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAACTTCTCTTATCGGAAATTCATAGTTTGAGACTAATAAGATT CAATACAAACAGAGATTTCACTGCTTCA	5354
	ATTTCCGATAAGAGAAG	5355
	CTTCTCTTATCGGAAAT	5356
25 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTTGATTGAATCTTATTAGTCTCAAACAT GAATTTCCGACAATAGAAGTTTGTAAGGTCAGTGTTCCAGATTTGT CTCATTGAATTCTAAGTCGTGAAGCTTA	5357
	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA CCTTACAACTTCTATTGTGCGGAAATTCATAGTTTGAGACTAATAA GATTCAATACAAACAGAGATTTCACTGCT	5358

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAAT <u>T</u> AGAAGTTT	5359
	AAACTTCTA <u>T</u> TTGTCCGA	5360
5 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACATGAA TTTCCGACAAGAGT <u>A</u> GTTTGTAAAGTCAGTGTTCCAGATTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT	5361
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAAACT <u>A</u> CTCTTGTCCGAAATTCATAGTTTGAGACTAA TAAGATTCAATACAAACAGAGATTTCCT	5362
	GACAAGAGT <u>A</u> GTTTGTGTA	5363
	TACAAACT <u>A</u> CTCTTGTGTC	5364
10 Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTGATTCTTCTTCACTTTC TCGGATCAGGTTTT <u>T</u> AAGATTGGAAGTCGGATAAGACTTCCTCCGA CGTGGAATATTCCGGTAAAAACGAGATTTC	5365
	GAATCTCGTTTTTACC G GAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTT <u>A</u> AAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAGCTTCACGACTTAGAATTCAATG	5366
	TCAGGTTTT <u>T</u> AAGATTGG	5367
	CCAATCTT <u>A</u> AAACCTGA	5368
15 20 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCT <u>A</u> AAGACGAGTTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTTC	5369
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCT CACAAACTCGTCTT <u>A</u> GCGGTGATTCATAACTTTAGCCAATGCATCA ACCTGCTCAACGTGGGGGATTGACTTCCA	5370
	ATCACCGCT <u>A</u> AAGACGAG	5371
	CTCGTCTT <u>A</u> GCGGTGAT	5372
25 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACT <u>A</u> GTTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTTCATGCTA	5373
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTG AAACCTCACAAACT <u>A</u> GTCTTGGCGGTGATTCATAACTTTAGCCAAT GCATCAACCTGCTCAACGTGGGGGATTGA	5374
	GCCAAGACT <u>A</u> GTTTGTG	5375
	CACAAACT <u>A</u> GTCTTGGC	5376

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTT T AGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTTCATGCTAAAGGTGGAGTCCACC	5377
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTC TGATTTCCAATCCT A AAACCTCACAACTCGTCTTGGCGGTGATTC ATAACTTTAGCCAATGCATCAACCTGCTC	5378
	TGAGGTTT T AGGATTGG	5379
	CCAATCCT A AAACCTCA	5380
10 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGT GAGGTTTCAGGATTGT T AAATCAGAGAGAAGCTCTGAGGGAAATTT TCATGCTAAAGGTGGAGTCCACCGAAGTAAA	5381
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAG CTTCTCTCTGATTT A CAATCCTGAAACCTCACAACTCGTCTTGGC GGTGATTCATAACTTTAGCCAATGCATCA	5382
	CAGGATTGT T AAATCAGA	5383
	TCTGATTT A CAATCCTG	5384
20 Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTG AGGTTTCAGGATTGGT T AATCAGAGAGAAGCTCTGAGGGAAATTT CATGCTAAAGGTGGAGTCCACCGAAGTAAAG	5385
	CTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGA GCTTCTCTCTGATT A CCAATCCTGAAACCTCACAACTCGTCTTGG CGGTGATTCATAACTTTAGCCAATGCATC	5386
	AGGATTGGT T AATCAGAG	5387
	CTCTGATT A CCAATCCT	5388
25 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCCTGG TGGAGATAATGATGT T AAAGAGAGGACAGATATGTTAGATTTAGGA CTGCAAATCAGAGCAATCTGTTATCTCAG	5389
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATA TCTGTCCTCTCTTT A CATCATTATCTCCACCAGGCGAACAGTTAGC AGCTAAGAGTGGTAGATCAATTCTTCAAG	5390
	TAATGATGT T AAAGAGAG	5391
	CTCTCTTT A CATCATT	5392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTG GAGATAATGATGGAATGAGAGGACAGATATGTTAGATTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	5393
	TCTCTGAGATAACAGATTGCTCTGATTGTCAGTCCTGAAATCTAAC ATATCTGTCCTCTCAATTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC	5394
	TGATGGAATGAGAGGAC	5395
	GTCCTCTCAATTCCATCA	5396
10 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAG ATAATGATGGAAAGATAGGACAGATATGTTAGATTTCAGGACTGCA AATCAGAGCAATCTGTTATCTCAGAGAACG	5397
	CGTTCTCTGAGATAACAGATTGCTCTGATTGTCAGTCCTGAAATCT AACATATCTGTCCTATCTTTCCATCATTATCTCCACCAGGCGAACA GTTAGCAGCTAAGAGTGGTAGATCAATTC	5398
	TGGAAAGATAGGACAGA	5399
	TCTGTCCTATCTTTCCA	5400
15 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATG ATGGAAAGAGAGGACTGATATGTTAGATTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT	5401
	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGTCAGTCCTG AAATCTAACATATCAGTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	5402
	GAGAGGACTGATATGTT	5403
	AACATATCAGTCCTCTC	5404
20 Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATGATGGA AAGAGAGGACAGATAGGTTAGATTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA	5405
	TGGTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTGTCAG TCCTGAAATCTAACCTATCTGTCCTCTCTTTCCATCATTATCTCCAC CAGGCGAACAGTTAGCAGCTAAGAGTGG	5406
	GACAGATAGGTTAGATT	5407
	AATCTAACCTATCTGTC	5408
25 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAATAATGTAGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT	5409
	AAGAAGAAGAAGAAGGTCGAGATGCTCAAGAAGAACGCGTTGTC TCTCGATCGCTTTCTACATTTTTTCCGCTGATTAAAGATAAAATTC GGATCTGTTGTTTTTCTCAGAGAAGGAT	5410

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	AAAAAATGTAGAAAGCG	5411
	CGCTTTCTACATTTTTT	5412
	CTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCAGC CGGAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTTCTTCTTG AGCATCTCCGACCTTCTTCTTCTTCTTCGC	5413
	GCGAAGAAGAAGAAGAAGGTCTGGAGATGCTCAAGAAGAACGCGT TGTCTCTCGATCGCTTACTCCATTTTTTCCGGCTGATTAAAGATAA AATTCGGATCTGTTGTTTTTCTCAGAGAAG	5414
10	AAATGGAGTAAGCGATC	5415
	GATCGCTTACTCCATT	5416
	GAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAA TGGAGAAAGCGATCTAGAGACAACGCGTTCTTCTTGAGCATCTCC GACCTTCTTCTTCTTCTTCGCACAATTACG	5417
	CGTAATTGTGCGAAGAAGAAGAAGGTCTGGAGATGCTCAAGAA GAACGCGTTGTCTCTAGATCGCTTTCTCCATTTTTTCCGGCTGATT AAAGATAAAATTCGGATCTGTTGTTTTTC	5418
15	AAGCGATCTAGAGACAA	5419
	TTGTCTCTAGATCGCTT	5420
	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGG AGAAAGCGATCGAGTGACAACGCGTTCTTCTTGAGCATCTCCGAC CTTCTTCTTCTTCTTCGCACAATTACGAGG	5421
	CCTCGTAATTGTGCGAAGAAGAAGAAGGTCTGGAGATGCTCAA GAAGAACGCGTTGTCACTCGATCGCTTTCTCCATTTTTTCCGGCT GATTAAAGATAAAATTCGGATCTGTTGTTTT	5422
20	CGATCGAGTGACAACGC	5423
	GCGTTGTCACTCGATCG	5424
	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGA AAGCGATCGAGAGATAACGCGTTCTTCTTGAGCATCTCCGACCTT CTTCTTCTTCTTCGCACAATTACGAGGCTT	5425
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGGTCTGGAGATGCT CAAGAAGAACGCGTTATCTCTCGATCGCTTTCTCCATTTTTTCCGG CTGATTAAAGATAAAATTCGGATCTGTTGT	5426
	TCGAGAGATAACGCGTT	5427
	AACGCGTTATCTCTCGA	5428

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTTCTCTCACAGCTTTTAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCT	5429
	AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	5430
	ACAGCTTTTAAGGCTCT	5431
	AGAGCCCTTAAAAGCTGT	5432
2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA	TTGAACATCTCCGTCCTTCTTCTTCTTCTCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTGAGCTTGCTTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGT	5433
	ACATCATCTCCATAGAGAGAGAGGTCTCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGAGCCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	5434
	CTCTGCTTGAGCTTGCT	5435
	AGCAAGCTCAAGCAGAG	5436
2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA	TCTCCGTCCTTCTTCTTCTTCTCTCTCACAGCTTTGAAGGCTCTCTCTGCTTCAGCTTGATTGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATT	5437
	AATGACTACATCATCTCCATAGAGAGAGAGGTCTCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGAGCCCTTCAAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5438
	TCAGCTTGATTGGCTGG	5439
	CCAGCCAATCAAGCTGA	5440
2,4-DB resistance glyoxysomal beta-ketoacyl-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG	TCCGTCCTTCTTCTTCTTCTCTCTCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTAGGCTGGGGACAGTGCTGCGTATCAGAGGACCTCTCTCTATGGAGATGATGTAGTCATTGT	5441
	ACAATGACTACATCATCTCCATAGAGAGAGAGGTCTCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGAGCCCTTCAAAGCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	5442
	AGCTTGCTAGGCTGGGG	5443
	CCCCAGCCTAGCAAGCT	5444

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG	TCACAGCTTTGAAGGCTCTCTCTGCTTCAGCTTGCTTGGCTGG GGACAGTGCTGCGTAGCAGAGGACCTCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA	5445
	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCCTCTGCTACGCAGCACTGTCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA	5446
	GCTGCGTAGCAGAGGAC	5447
	GTCCTCTGCTACGCAGC	5448
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTC TTCTTCTCACAATTAGGAGTCCGCTCTTGCCGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT	5449
	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTCCTAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGCAACACTTGCTGTCTGTTG	5450
	CACAATTAGGAGTCCGC	5451
	GCGGACTCCTAATTGTG	5452
15 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT CTTCTCACAATTACTAGTCCGCTCTTGCCGCATCAGTATGTGCTG CAGGGGATAGCGCCGCATATCATAGGGCTT	5453
	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACTAGTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	5454
	ACAATTACTAGTCCGCT	5455
	AGCGGACTAGTAATTGT	5456
20 25 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC CGCTCTTGCCGCATGAGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTTCTGTTTATGGAGACGATGT	5457
	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC CCTGCAGCACATACTCATGCGGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	5458
	TGCCGCATGAGTATGTG	5459
	CACATACTCATGCGGCA	5460

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATGAGCTGCAGGGGATAGCGCCGCATATCATAG GGCTTCTGTTTATGGAGACGATGTGGTGATT	5461
	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC GCTATCCCCTGCAGCTCATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	5462
	TCAGTATGAGCTGCAGG	5463
	CCTGCAGCTCATACTGA	5464
10 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTTATGGAGACGATGT GGTGATTGTGGCAGCTCATCGTACTGCACTT	5465
	AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATA AACAGAAGCCCTATGCTATGCGGCGCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA	5466
	GCCGCATAGCATAGGGC	5467
	GCCCTATGCTATGCGGC	5468
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG	GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCC TTCTTCTTCCGCTTAGACAAATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA	5469
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATTTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATCGCCTTC	5470
	TCCGCTTAGACAAATGA	5471
	TCATTTGTCTAAGCGGA	5472
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTT CCGCTTACACAAATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCTTCGTATCAAAGGACAT	5473
	ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATTTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	5474
	ACACAAATTAATCTTCG	5475
	CGAAGATTAAATTTGTGT	5476

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG	GGCAGAGCATTTTGTACATCATCTCCGGCCTTCTTCTTCCGCTTA CACAAATGAATCTT <u>A</u> GCTCTCTGCATCGGTTTGTGCAGCTGGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	5477
	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCT <u>A</u> AGATTCAATTTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	5478
	TGAATCTT <u>A</u> GCTCTCTG	5479
	CAGAGAGCT <u>A</u> AGATTCA	5480
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATC TTCGCTCTCTGCAT <u>A</u> GGTTTGTGCAGCTGGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTTGGAGATGATGT	5481
	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC CAGCTGCACAAACCT <u>A</u> TGCAGAGAGCGAAGATTCAATTTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	5482
	CTCTGCAT <u>A</u> GGTTTGTG	5483
	CACAAACCT <u>A</u> TGCAGAG	5484
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTC TCTGCATCGGTTT <u>A</u> GCAGCTGGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTTGGAGATGATGTCGTGATT	5485
	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA CTATCCCCAGCTGCT <u>C</u> AAACCGATGCAGAGAGCGAAGATTCAATTT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	5486
	TCGGTTT <u>G</u> AGCAGCTGG	5487
	CCAGCTGCT <u>C</u> AAACCGA	5488
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTTCGGCTT <u>A</u> GAGCCATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCGTCGTATCAA	5489
	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATGGCT <u>C</u> TAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	5490
	TCGGCTT <u>A</u> GAGCCATGA	5491
	TCATGGCT <u>C</u> TAAGCCGA	5492

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATAGCCATTAAATCTTCGCTCTCTGCATCGGTTTGTGCAG CTGGGGATAGTGCGTCGTATCAAAGAACGT	5493
	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGTAGCAGAATGCTCTGCCTGTTGAT	5494
	ATAGCCATTAAATCTTCG	5495
	CGAAGATTAAATGGCTAT	5496
10 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTT ATAGCCATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGG ATAGTGCGTCGTATCAAAGAACGTCGGTGTT	5497
	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAA GGCCGGAGATGATGTAGCAGAATGCTCTGCC	5498
	TGAATCTTAGCTCTCTG	5499
	CAGAGAGCTAAGATTCA	5500
15 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATC TTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTA TCAAAGAACGTCGGTGTTTGGAGATGATGT	5501
	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	5502
	CTCTGCATAGGTTTGTG	5503
	CACAAACCTATGCAGAG	5504
20 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Cys33Term TGT-TGA	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTC TCTGCATCGGTTTGAGCAGCTGGGGATAGTGCGTCGTATCAAAGA ACGTCGGTGTTTGGAGATGATGTCGTGATA	5505
	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGG CTATAAGCCGAAGATGAAGGCCGGAGATGA	5506
	TCGGTTTGAGCAGCTGG	5507
	CCAGCTGCTCAAACCGA	5508
25 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln5Term CAG-TAG	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTG CTATGGCAACTCATAGCAAACGCAACCTCCTTCGATTTTCCCG CTCTTGCCGATGAAAATCCAGATTCCAG	5509
	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAAG GAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCTT GGAAGAATCCAAGCGGCAAAAGAGACTATGA	5510

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAACTCATTAGCAAACG	5511
	CGTTTGCTAATGAGTTG	5512
5 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA	TAGTCTCTTTT GCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAGTAAACGCAACCTCCTTCCGATTTTCCCGCTC TTGCCGATGAAAATCCCAGATTCCAGGTT	5513
	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGG AAGGAGGTTGCGTTTACTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAGAATCCAAGCGGCAAAAGAGACTA	5514
	CTCATCAGTAAACGCAA	5515
	TTGCGTTTACTGATGAG	5516
10 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACGTAACCTCCTTCCGATTTTCCCGCTCTTGCC GATGAAAATCCCAGATTCCAGGTTCAATTT	5517
	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAA AATCGGAAGGAGGTTACGTTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTTGGAAGAATCCAAGCGGCAAAAG	5518
	AGCAAACGTAACCTCCT	5519
	AGGAGGTTACGTTTGCT	5520
15 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTT CCCGCTCTTGCCGATTAAAATCCCAGATTCCAGGTTCAATTTACA CCTTCTAATCATTATTTCTTAATTTTCTT	5521
	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG AATCTGGGAATTTTAATCGGCAAGAGCGGGAAAATCGGAAGGAG GTTGCGTTTGCTGATGAGTTGCCATAGCAGC	5522
	TTGCCGATTAAAATTCC	5523
	GGAATTTTAATCGGCAA	5524
20 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT GCCGATGAAAATTCCTAGATTCCAGGTTCAATTTACACCTTCTAAT CATTATTTCTTAATTTTCTTTGGTGGATT	5525
	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATT GAACCTGGAATCTAGGAATTTTCATCGGCAAGAGCGGGAAAATCG GAAGGAGGTTGCGTTTGCTGATGAGTTGC	5526
	AAAATTCCTAGATTCCA	5527
	TGGAATCTAGGAATTTT	5528

Example 8**Production of albino mutants for the analysis of photosynthetic processes**

Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 18
Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 10 White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG ATGGCGGCGGATTTGAGGCATCTCCTCTGGTACGTTGACGATTTC CGGCCTTTGGTTACTCTTCGACGCTCTAG	5529
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCTCAAATCGCCGCCATCTCCGTCAGGAACCAA AGATTTGAGCAGATAATTTACAGGAAAGAA	5530
	GGCGATTTGAGGCATCT	5531
	AGATGCCTCAAATCGCC	5532
15 White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCA TCTCCTCTGGTACGTAGACGATTTACAGGCCTTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTTCGTACAGCTC	5533
	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAA GGCCGTGAAATCGTCTACGTACCAGAGGAGATGCCTGAAATCGCC GCCATCTCCGTCAGGAACCAAAGATTTGAGC	5534
	TGGTACGTAGACGATTT	5535
	AAATCGTCTACGTACCA	5536
20 White leaves Immutans <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCATCTCCTCTG GTACGTTGACGATTTGACGGCCTTTGGTTACTCTTCGACGCTCTAG AGCCGCCGTTTCGTACAGCTCCTCTCACCG	5537
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGTCAAATCGTCAACGTACCAGAGGAGATGCC TGAAATCGCCGCCATCTCCGTCAGGAACCAAA	5538
	GACGATTTGACGGCCTT	5539
	AAGGCCGTCAAATCGTC	5540
25 White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA	GCGGCGATTTACAGGCATCTCCTCTGGTACGTTGACGATTTACGG CCTTTGGTTACTCTTTGACGCTCTAGAGCCGCCGTTTCGTACAGCT CCTCTACCGATTGCTTCATCATCTTCCTC	5541
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTCAAAGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCAGAGGAGATGCCTGAAATCGCCGC	5542
	TTACTCTTTGACGCTCT	5543
	AGAGCGTCAAAGAGTAA	5544

5	White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTTACGGCCTTTGGTTA	5545
		CTCTTCGACGCTCTTGAGCCGCCGTTTCGTACAGCTCCTCTCACC	
		GATTGCTTCATCATCTTCCTCTCTCTCTC	
		GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG	5546
10	White leaves Immutans <i>Lycopersicon</i> <i>esculentum</i> Gly11Term GGA-TGA	TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG	
		TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	
		GACGCTCTTGAGCCGCC	5547
		GGCGGCTCAAGAGCGTC	5548
15	White leaves Immutans <i>Lycopersicon</i> <i>esculentum</i> Ser13Term TCA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTGATTT	5549
		CTGCTATGAGTTTTTGAACTCAGTTTCTTCATATTCTTGTTTTAGA	
		GCTAGGAGTTTTGAGAAGTCATCAGTTT	
		AACTGATGACTTCTCAAACTCCTAGCTCTAAACAAGAATATGAA	5550
20	White leaves Immutans <i>Lycopersicon</i> <i>esculentum</i> Ser16Term TCA-TGA	GAACTGAGGTTCAAACTCATAGCAGAAATCGAAATCGCCATTCT	
		TTGATCCTTCTTCTTCCCACAAGAATC	
		TGAGTTTTTGAACTCA	5551
		TGAGGTTCAAACTCA	5552
25	White leaves Immutans <i>Lycopersicon</i> <i>esculentum</i> Tyr17Term TAT-TAG	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTGATTTCTGCTA	5553
		TGAGTTTTGGAACCTGAGTTTCTTCATATTCTTGTTTTAGAGCTAGG	
		AGTTTTGAGAAGTCATCAGTTTATGCAA	
		TTGCATAAACTGATGACTTCTCAAACTCCTAGCTCTAAACAAGA	5554
		ATATGAAGAACTCAGGTTCCAACTCATAGCAGAAATCGAAATC	
		GCCATTCTTGATCCTTCTTCTTCCCAC	
		TGGAACCTGAGTTTCTT	5555
		AAGAACTCAGGTTCCA	5556
		AAGAAGGATCAAGAATGGCGATTTGATTTCTGCTATGAGTTTTGG	5557
		AACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA	
		AGTCATCAGTTTATGCAATTCCCAGAA	
		TTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTAGCTC	5558
		TAAACAAGAATATCAAGAACTGAGGTTCCAACTCATAGCAGA	
		AATCGAAATCGCCATTCTTGATCCTTCTT	
		AGTTTCTTGATATTCTT	5559
		AAGAATATCAAGAACT	5560
		AGGATCAAGAATGGCGATTTGATTTCTGCTATGAGTTTTGGAACC	5561
		TCAGTTTCTTCATAGTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC	
		ATCAGTTTATGCAATTCCCAGAACCCA	
		TGGGTTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTA	5562
		GCTCTAAACAAGACTATGAAGAACTGAGGTTCCAACTCATAG	
		CAGAAATCGAAATCGCCATTCTTGATCCT	
		TCTTCATAGTCTTGTTT	5563
		AAACAAGACTATGAAGA	5564

5	White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA	AAGAATGGCGATTTCTGATTTCTGCTATGAGTTTTGGAACCTCAGTT TCTTCATATTCTTGATTTAGAGCTAGGAGTTTTGAGAAGTCATCAGT TTTATGCAATTCCTCAGAACCCATGTCCG	5565
		CCGACATGGGTTCTGGGAATTGCATAAACTGATGACTTCTCAAAA CTCCTAGCTCTAAATCAAGAATATGAAGAACTGAGGTTCCAAAAC TCATAGCAGAAATCGAAATCGCCATTCTT	5566
		TATTCTTGATTTAGAGC	5567
		GCTCTAAATCAAGAATA	5568
10	White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTAT GAGTTTTCGAACTTGAGTTTCTTCTTCATATTCAGCATTTTTGTGCA ATTCCAAGAACCCATTTTGTGGAATTC	5569
		GAATTCAAACAAAATGGGTTCTTGGGAATTGCACAAAATGCTGAAT ATGAAGAAGAACTCAAGTTTCGAAAACCTCATAGCAGATATGGAAAT CGCCATTCTTGATTTTTTATCGGACGCG	5570
		TCGAACTTGAGTTTCTT	5571
		AAGAACTCAAGTTCTGA	5572
15	White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACT TCAGTTTCTTCTTGATATTCAGCATTTTTGTGCAATTCGAAGAACCC ATTTTGTGGAATTCCTATTTTCACT	5573
		AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGGAATTGCACA AAAATGCTGAATATCAAGAAGAACTGAAGTTTCGAAAACCTCATAGC AGATATGGAAATCGCCATTCTTGATTTTT	5574
		TTCTTCTTGATATTCAG	5575
		CTGAATATCAAGAAGAA	5576
20	White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGT TTCTTCTTCATATTGAGCATTTTTGTGCAATTCGAAGAACCCATTTT GTTTGAATTCTCTATTTTCACTTAGGAA	5577
		TTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGGAATT GCACAAAATGCTCAATATGAAGAAGAACTGAAGTTTCGAAAACCTC ATAGCAGATATGGAAATCGCCATTCTTG	5578
		TTTCATATTGAGCATTTT	5579
		AAAATGCTCAATATGAA	5580
25	White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG	CGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCA TATTCAGCATTTTAGTGCAATTCGAAGAACCCATTTTGTGGAATTC TCTATTTTCACTTAGGAATTCTCATAG	5581
		CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTT CTTGGGAATTGCACTAAAATGCTGAATATGAAGAAGAACTGAAGTT CGAAAACCTCATAGCAGATATGGAAATCG	5582
		AGCATTTTAGTGCAATT	5583
		AATTGCACTAAAATGCT	5584

5	White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATT CAGCATTTTTGTGA <u>A</u> AATTCCAAGAACCCATTTTGTGGAATTCTCTA TTTTCACTTAGGAATTCTCATAGAACT	5585
		AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATG GGTTCTTGGAATTTCACAAAAATGCTGAATATGAAGAAGAACTGA AGTTCGAAAACATCATAGCAGATATGGAA	5586
		TTTTGTGA <u>A</u> AATTCCA	5587
		TTGGAATTTCACAAAA	5588
10	White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG	TTCCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGG AGTCCTTCCCCTTCAGGTAGACGGCTCCTCCTGACGAGCCACTGG TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	5589
		CGAGCTTAACCAACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCG TCAGGAGGAGCCGTCT <u>A</u> CCTGAAGGGGAAGGACTCCTCGACGGC CACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	5590
		CCTTCAGGTAGACGGCT	5591
		AGCCGTCT <u>A</u> CCTGAAGG	5592
15	White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGA GACGGCTCCTCCTGACTAGCCACTGGTCACCGCCGAGGAGAGCT GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	5593
		AAATGTTACGGACTGCTCGAGCTTAACCAACCCAGCTCTCCTCGG CGGTGACCAGTGGCT <u>A</u> GTGAGGAGGAGCCGTCTCCCTGAAGGGG AAGGACTCCTCGACGGCCACCTCGGTCTGCTC	5594
		CTCCTGACTAGCCACTG	5595
		CAGTGGCTAGTCAGGAG	5596
20	White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGA GCCACTGGTCACCGCCTAGGAGAGCTGGGTGGTTAAGCTCGAGC AGTCCGTGAACATTTTCTCACGGAGTCAGTCA	5597
		TGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCTTAA CCACCCAGCTCTCCTAGGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	5598
		TCACCGCCTAGGAGAGC	5599
		GCTCTCCTAGGCGGTGA	5600
25	White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCAGT CCGTGAACATTTTCTCACGGAGTCAGTCATCA	5601
		TGATGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCT TAACCAACCCAGCTCTACTCGGCGGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	5602
		CCGCCGAGTAGAGCTGG	5603
		CCAGCTCTACTCGGCGG	5604

5	White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA TTTTCTCACGGAGTCAGTCATCACGATACTT	5605
		AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTACGGACTG CTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	5606
		GAGAGCTGAGTGGTTAA	5607
		TTAACCACTCAGCTCTC	5608
10	White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA	TCCGGAGGAGGAAGGGGGATTGACGAGGAGCTCACCCTCGCCG GCGAGGACGGCGACTGAGTCGTGAGATTGAGCAGTCCTTCAAC GTATTCCTCACGGATACTGTCATCTTTATACTC	5609
		GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG CTCGAATCTGACGACTCAGTCGCCGTCTCGCCGGCGAGGGTGA GCTCCTCGTCGAATCCCCCTTCCTCCTCCGA	5610
		GGCGACTGAGTCGTGAG	5611
		CTGACGACTCAGTCGCC	5612
15	White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA	GAGGAAGGGGGATTGACGAGGAGCTCACCCTCGCCGGCGAGG ACGGCGACTGGGTCGTCTGATTGAGCAGTCCTTCAACGTATTCC TCACGGATACTGTCATCTTTATACTCGATATTC	5613
		GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAA GGACTGCTCGAATCAGACGACCCAGTCGCCGTCTCGCCGGCGA GGGTGAGCTCCTCGTCGAATCCCCCTTCCTC	5614
		GGGTCGTCTGATTGAG	5615
		CTCGAATCAGACGACCC	5616
20	White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG	GGGGGATTGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCG ACTGGGTCGTGAGATTCTAGCAGTCCTTCAACGTATTCTCACGGA TACTGTCATCTTTATACTCGATATTCTGTATC	5617
		GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAC GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCTCGCC GGCGAGGGTGAGCTCCTCGTCGAATCCCCC	5618
		TCAGATTCTAGCAGTCC	5619
		GGACTGCTAGAATCTGA	5620
25	White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG	GGATTGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTG GGTCGTGAGATTGAGTAGTCCTTCAACGTATTCTCACGGATACT GTCATCTTTATACTCGATATTCTGTATCGTG	5621
		CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCTC GCCGGCGAGGGTGAGCTCCTCGTCGAATCC	5622
		GATTGAGTAGTCCTTC	5623
		GAAGGACTACTCGAATC	5624

5

White leaves Immutans <i>Triticum aestivum</i> Tyr46Term TAT-TAG	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA CTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTG CTCGAGACCATCGCCAGGGTGCCCTATTTTC	5625
	GAAATAGGGCACCCTGGCGATGGTCTCGAGCACGAAGAACCTTG CGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG	5626
	ATTCTGTAGCGTGACCG	5627
	CGGTCACGCTACAGAAT	5628

Example 9**Altering amino acid content of plants**

Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 19
Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 10 Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTTCTCCTAATTTTCGTCCGTCAGCT GAGCATTAAAGCCC <u>A</u> TAGAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAACCC	5629
	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTTCTA <u>T</u> GGGCTTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAAATCTTAAGATCCTGGAGGATA	5630
	TAAAGCCC <u>A</u> TAGAACT	5631
	AGTTTCTA <u>T</u> GGGCTTTA	5632
15 Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC	TCTTAAGATTTCTCCTAATTTTCGTCCGTCAGCTGAGCATTAAAGC CCGTAGAACTGTAA <u>A</u> CAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCGCGTT	5633
	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTG <u>T</u> TACAGTTTCTACGGGCTTTAATGCTCAGC TGACGGACGAAATTAGGAGGAAATCTTAAGA	5634
	AAACTGTAA <u>A</u> CAACATCG	5635
	CGATGTTG <u>T</u> TACAGTTT	5636
20 Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT	TTTCCTCCTAATTTTCGTCCGTCAGCTGAGCATTAAAGCCCCTAGAA ACTGTAGCAACATC <u>A</u> GTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCGCGTTACCTTCGG	5637
	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACT <u>T</u> GATGTTGCTACAGTTTCTACGGGCTTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAAA	5638
	GCAACATC <u>A</u> GTGTTGCA	5639
	TGCAACACT <u>T</u> GATGTTGC	5640
25 Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT	TTCCTCCTAATTTTCGTCCGTCAGCTGAGCATTAAAGCCCCTAGAAA CTGTAGCAACATCG <u>A</u> TGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAACCCATCCTCCGCGTTACCTTCGGC	5641
	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACAT <u>C</u> GATGTTGCTACAGTTTCTACGGGCTTTA ATGCTCAGCTGACGGACGAAATTAGGAGGAA	5642
	CAACATCG <u>A</u> TGTTGCAC	5643
	GTGCAACAT <u>C</u> GATGTTG	5644

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Met Overproduction CGS <i>Fragraria vesca</i> Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCCCAACCGCAACTGCAGCAACATCGGCGTTCGCG CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	5645
	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCGGTGGGCCTTGGTGCTGAGCTGGCGGACGA AGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	5646
	CAAGGCCCAACCGCAACT	5647
	AGTTGCGGTGGGCCTTG	5648
10 Met Overproduction CGS <i>Fragraria vesca</i> Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAG GCCCGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGC GGCTTCGTGGTCCAACAAAGACTCCGACCTTTC	5649
	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTG CGCGACGCCGATGTTGTTGCAGTTGCGGCGGGCCTTGGTGCTGA GCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	5650
	CAACTGCAACAACATCG	5651
	CGATGTTGTTGCAGTTG	5652
15 Met Overproduction CGS <i>Fragraria vesca</i> Gly80Ser GGC-AGC	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	5653
	GCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCG ACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGGGCCTT GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5654
	GCAACATCAGCGTCGCG	5655
	CGCGACGCTGATGTTGC	5656
20 Met Overproduction CGS <i>Fragraria vesca</i> Gly80Asp GGC-GAC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGTG GTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	5657
	GGCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCG GACGATCTGCGCGACGCTCGATGTTGCTGCAGTTGCGGCGGGCCT TGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	5658
	CAACATCAGCGTCGCGC	5659
	GCGCGACGCTCGATGTTG	5660
25 Met Overproduction CGS <i>Glycine max</i> Arg68His CGC-CAC	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGC TAAGCACCAAGGCGAGCCGCAACTGCAGCAACATCGGCGTTCGCG CAAATCGTCGCCGCTTCGTGGTCAACAACAG	5661
	CTGTTGTTGACACGAAGCGGCGACGATTTGCGCGACGCCGAT GTTGCTGCAGTTGCGGCTCGCCTTGGTGCTTAGCTGGCGCTGGA AGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	5662
	CCAAGGCGAGCCGCAAC	5663

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGC <u>TCGC</u> CTTGG	5664
5 Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAG GCGCGCCGCAACTGCA <u>ACA</u> ACATCGGCGTCGCGCAAATCGTCGC CGCTTCGTGGTCTGAACAACAGCGACAACCTCTCC	5665
	GGAGAGTTGTCGCTGTTGTTGACCACGAAGCGGCGACGATTTG CGCGACGCCGATGTTG <u>TTG</u> CAGTTGCGGCGCGCCTTGTTGCTTA GCTGGCGCTGGAAGTTGGAGGGAAGCGGAGGA	5666
	CAACTGCA <u>ACA</u> ACATCG	5667
	CGATGTTG <u>TTG</u> CAGTTG	5668
10 Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG CAACTGCAGCAACATC <u>AG</u> CGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACAACCTCTCCGGCCGCCG	5669
	CGGCGGCCGGAGAGTTGTCGCTGTTGTTGACCACGAAGCGGC GACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5670
	GCAACATC <u>AG</u> CGTCGCG	5671
	CGCGACGCTGATGTTGC	5672
15 Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG AACTGCAGCAACATCG <u>AG</u> CGTCGCGCAAATCGTCGCCGCTTCGT GTGCAACAACAGCGACAACCTCTCCGGCCGCCG	5673
	CCGGCGGCCGGAGAGTTGTCGCTGTTGTTGACCACGAAGCGGC GACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	5674
	CAACATCG <u>AG</u> CGTCGCG	5675
	GCGCGACGCTGATGTTG	5676
20 Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC	TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTCTGTAGGCAGCT AAGCATTAAAGGCT <u>CAC</u> AGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGGCTTCCTGGTCTAACAACCA	5677
	TGGTTGTTAGACCAGGAAGCCGCCACAACCTTGAGCCACGCCAATA TTGCTGCAATTCCT <u>GTG</u> AGCCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAAATCAGAGAAGACA	5678
	TAAGGCT <u>CAC</u> AGGAATT	5679
	AATTCCT <u>GTG</u> AGCCTTA	5680
25 Met Overproduction CGS <i>Solanum tuberosum</i> Ser74Asn AGC-AAC	TTTTCAGGTTTCCTCCTAATTTCTGTAGGCAGCTAAGCATTAAAGC TAGGAGGAATTGCA <u>ACA</u> ATATTGGCGTGGCTCAAGTTGTGGCGG CTTCCTGGTCTAACAACCAAGCCGGTCCTGA	5681
	TCAGGACCGGCTTGTTGTTAGACCAGGAAGCCGCCACAACCTTG AGCCACGCCAATATTG <u>TTG</u> CAATTCCTCCTAGCCTTAATGCTTAGC TGCTCACGAAATTAGGAGGAAACCTGAAAA	5682

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	GAATTGCA <u>A</u> CAATATTG	5683
	CAATATTG <u>T</u> GCAATTC	5684
	TTTCCTCCTAATTTCTGTGAGGCAGCTAAGCATTAAAGGCTAGGAGG AATTGCAGCAATATT <u>A</u> GCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTACAACCAAGCCGGTCTCTGAATTCCTC	5685
	GAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCC ACAACCTTGAGCCACGCT <u>A</u> AATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	5686
	GCAATATT <u>A</u> GCGTGGCT	5687
10	AGCCACGCT <u>A</u> AATATTGC	5688
	TTTCCTCCTAATTTCTGTGAGGCAGCTAAGCATTAAAGGCTAGGAGGA ATTGCAGCAATATTG <u>A</u> GCGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTACAACCAAGCCGGTCTCTGAATTCCTC	5689
	GGAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGC CACAACCTTGAGCCACGCT <u>A</u> CAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	5690
	CAATATTG <u>A</u> GCGTGGCTC	5691
	GAGCCACGCT <u>A</u> CAATATTG	5692
15	CTTCCTCTCTTATCCTTCGCTTTCTCCCACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCC <u>A</u> CAACTGCAGCAACATTGGTGTGCGAC AGGTCGTCGCTGCCTCCTGGTCCAACAACCTC	5693
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTG <u>T</u> GGCGAGCCTTGGTGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	5694
	GGCTCGCC <u>A</u> CAACTGCA	5695
	TGCAGTTG <u>T</u> GGCGAGCC	5696
20	TCCTTCGCTTTCTCCCACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCA <u>A</u> CAACATTGGTGTGCGACAGGTCGTCTGCT GCCTCCTGGTCCAACAACCTCCGATGCCGGCGC	5697
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTG <u>T</u> TGCAGTTGCGGCGAGCCTTGGTGTCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	5698
	CAACTGCA <u>A</u> CAACATTG	5699
	CAATGTTG <u>T</u> TGCAGTTG	5700

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Ser GGT-AGT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGC AACTGCAGCAACATTAGTGTGCGACAGGTCGTGCTGCCTCCTG GTCCAACAACCTCCGATGCCGGCGCCACCTCTT	5701
	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAGTTGCGGCGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	5702
	GCAACATTAGTGTGCGA	5703
	TGCGACACTAATGTTGC	5704
10 Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Asp GGT-GAT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCA ACTGCAGCAACATTGATGTGCGACAGGTCGTGCTGCCTCCTGG TCCAACAACCTCCGATGCCGGCGCCACCTCTTG	5705
	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGCGGCGAGCC TTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	5706
	CAACATTGATGTGCGAC	5707
	GTGCGACATCAATGTTG	5708
15 Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGC TTAGCACCAAGGCACACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	5709
	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGA TGTTGCTGCAGTTGCGGTGTGCCTTGGTGCTAAGCTGGCGGACA AAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	5710
	CAAGGCACACCGCAACT	5711
	AGTTGCGGTGTGCCTTG	5712
20 Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGG CACGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCC GCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	5713
	GGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGGCGACGATC TGCGCGACGCCGATGTTGTGTCAGTTGCGGCGTGCCTTGGTGCT AAGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	5714
	CAACTGCAACAACATCG	5715
	CGATGTTGTGTCAGTTG	5716
25 Met Overproduction CGS <i>Zea mays</i> Gly48Ser GGC-AGC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCACTTAG	5717
	CTAAGTGGGGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGG CGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTGCC TTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	5718
	GCAACATCAGCGTCGCG	5719

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGCGACGCTGATGTTGC	5720
Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCGACGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCCACTTAGG	5721
	CCTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCG GCGACGATCTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGTGC CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	5722
	CAACATCGACGTCGCGC	5723
	GCGCGACGTCGATGTTG	5724
Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG GAAGTTTCAAGGATCGTGGAATGACTGTTTTGGTTAGTCAAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	5725
	ACCACAGGTCGTTTCATCTTCTCAGACGATTAACCTTACTAATCCA AAACAGTCATTCCACGATCCTTGAAACTTCCTGTATGACTAATCCC ACAGTGTTTCACCCACAGATCATTATAC	5726
	CAAGGATCGTGGAATGA	5727
	TCATTCCACGATCCTTG	5728
Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG GTAGTTTTAAGGATCGTGGGATGACTGTTTTGGTGAGTCAAGTTAA TCGCTTGCGGAAAATGCATAAACCGGTTGT	5729
	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACCTTACTCACCA AAACAGTCATCCCACGATCCTTAAACTACCAGTATGGCTAATCCC ACAGTGTTTGACCCACAAATCAGTCATGC	5730
	TAAGGATCGTGGGATGA	5731
	TCATCCCACGATCCTTA	5732
Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC	TCATTGGGCACACAGTGAAGTCTTTGGCTCTAGAATCAAAGTGA TAGGCAACACAGGAAACAACCTCAACAGAGAAGCCGTCCACGCA ACAGAACAGGGATTTGCTGTTGGCATGCATGC	5733
	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT TCTCTGGTTGAGTTGTTTCTGTGTTGCCTATCACTTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCCAATGA	5734
	CACAGGAAACAACCTCAA	5735
	TTGAGTTGTTTCTGTG	5736
Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA GAGAAGCCGTCCACGAAACAGAACAGGGATTTGCTGTTGGCATG CATGCGGCTCTCCACATCAATCCTTACTACGG	5737
	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AAATCCCTGTTCTGTTTCGTGGACGGCTTCTCTGGTTGAGTTGCTT CCTGTGTTGCCTATCACTTTGATTCTAGAGC	5738

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CGTCCACGAAACAGAAC	5739
	GTTCTGTTTCGTGGACG	5740
Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCACAACAACAGAACAGGGATTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG	5741
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCAA ATCCCTGTTCTGTTGTGTGGACGGCTTCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTTGATTCTAGAGCC	5742
	CCGTCCACAACAACAGAA	5743
	TTCTGTTGTGTGGACGG	5744
Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT CGGCAACACAGGAAATAACTCAACAAGGGAGGCTATTCACGCAAC TGAGCAGGGATTGCTGTAGGTATGCACGC	5745
	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTTGTTGAGTTATTTCTGTGTTGCCGACCACTTTAATTTTAGT GCCAAAGCAGTTAACTGTATGCCCAATAA	5746
	CACAGGAAATAACTCAA	5747
	TTGAGTTATTTCTGTG	5748
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAAGTCAACAA GGGAGGCTATTCACGTAAGTGAAGCAGGGATTGCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG	5749
	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC GAATCCCTGCTCAGTTACGTGAATAGCCTCCCTTGTTGAGTTACTT CCTGTGTTGCCGACCACTTTAATTTTAGTGC	5750
	TATTCACGTAAGTGAAGC	5751
	GCTCAGTTACGTGAATA	5752
Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACA AGGGAGGCTATTCACAACAAGTGAAGCAGGGATTGCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG	5753
	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG AATCCCTGCTCAGTTGTGTGAATAGCCTCCCTTGTTGAGTTACTTC CTGTGTTGCCGACCACTTTAATTTTAGTGCC	5754
	CTATTCACAACAAGTGAAG	5755
	CTCAGTTGTGTGAATAG	5756
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ser165Asn AGT-AAT	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT AGGCAACACGGGAAATAACTCAACCAGAGAAGCTGTTACGCGA CAGAGCAGGGATTGCTGTTGGCATGCATGC	5757

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCT TCTCTGGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCCGATGA	5758
	CACGGGAAATAACTCAA	5759
	TTGAGTTATTTCCCGTG	5760
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCA GAGAAGCTGTTACAGTGACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG	5761
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCAACGTGAACAGCTTCTCTGGTTGAGTTACTT CCCGTGTTGCCTATCACTTTAATGTTGGCTC	5762
	TGTTACAGTGACAGAGC	5763
	GCTCTGTCAACGTGAACA	5764
Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC AGAGAAGCTGTTACACACGACAGAGCAGGGATTTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACG	5765
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTCTGTGAACAGCTTCTCTGGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTGGCTCC	5766
	CTGTTACACACGACAGAG	5767
	CTCTGTCTGTGAACAG	5768
Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT	TCATCGGGCACACTGTAACTGCTTTGGAACAACTAAAGTGAT AGGCAACACGGGAAATAACTCAACTAGAGAAGCGATTACAGCTTC AGAGCAGGGATTTGCTGTTGGCATGCATGC	5769
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA	5770
	CACGGGAAATAACTCAA	5771
	TTGAGTTATTTCCCGTG	5772
Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA GAGAAGCGATTACAGTTTCAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG	5773
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAAACGTGAATCGCTTCTCTAGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTAGTTC	5774
	GATTCACGTTTCAGAGC	5775
	GCTCTGAAACGTGAATC	5776

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT	GGAACAACTAAAGTGATAGGCAACACGGGAAGTAACTCAACT AGAGAAGCGATTACACTTCAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	5777
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAGTGTGAATCGCTTCTCTAGTTGAGTTACTTCC CGTGTTCCTATCACTTTAATGTTAGTTCC	5778
	CGATTCACACTTCAGAG	5779
	CTCTGAAGTGTGAATCG	5780
10 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAAGTCTTTGGCTCTAGAATTAAGTGA TAGGCAACACAGGAAATAACTCAACCAGAGAAGCTGTTACGCAA CAGAGCAGGGATTTGCTGTTGGCATGCATG	5781
	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTT CTCTGGTTGAGTTATTTCTGTGTTGCCTATCACTTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCAATGAG	5782
	CACAGGAAATAACTCAA	5783
	TTGAGTTATTTCTGTG	5784
15 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA	GCTCTAGAATTAAGTGATAGGCAACACAGGAAGTAACTCAACCA GAGAAGCTGTTACGTAACAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	5785
	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTTACGTGAACAGCTTCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTTAATTCTAGAGC	5786
	TGTTACGTAACAGAGC	5787
	GCTCTGTTACGTGAACA	5788
20 Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA	GGCTCTAGAATTAAGTGATAGGCAACACAGGAAGTAACTCAACC AGAGAAGCTGTTACACAACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	5789
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTTGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC TGTGTTGCCTATCACTTTAATTCTAGAGCC	5790
	CTGTTACACAACAGAG	5791
	CTCTGTTGTGTGAACAG	5792
25 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCAT CGGGAACACTGGAAACAACCTCCACAAGGGAAGCAATCCATGCAA CTGAACAGGGATTTGCTGTAGGTATGCATGC	5793
	GCATGCATACCTACAGCAAATCCCTGTTCAAGTTGCATGGATTGCTT CCCTTGTGGAGTTGTTCCAGTGTTCCCGATGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA	5794
	CACTGGAAACAACCTCCA	5795

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGAGTTGTTCCAGTG	5796
5 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA GGAAGCAATCCATGTAAGTGAACAGGGATTTGCTGTAGGTATGC ATGCAGCTCTTCACATTAATCCCTACTATGG	5797
	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTTCAAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC CAGTGTTCCTGATGACTTTGATGGACCCTC	5798
	AATCCATGTAAGTGAAC	5799
	GTTCAAGTTACATGGATT	5800
10 Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC AAGGGAAGCAATCCATACAAGTGAACAGGGATTTGCTGTAGGTAT GCATGCAGCTCTTCACATTAATCCCTACTATG	5801
	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTTCAAGTTGATGGATTGCTTCCCTTGTGGAGTTGCTTCC AGTGTTCCTGATGACTTTGATGGACCCTCC	5802
	CAATCCATACAAGTGAAC	5803
	TTCAGTTGATGGATTG	5804
15 Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT TGGAACACTGGAAACAATTCGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATTCGCGGTTGGAATGCATGC	5805
	GCATGCATTCCAACCGCGAATCCTTGTTCAAGTCGCGTGGATTGCT TCTCTAGTCGAATTGTTCCAGTGTTTCCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	5806
	CACTGGAAACAATTCGA	5807
	TCGAATTGTTCCAGTG	5808
20 Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA GAGAAGCAATCCACGTGACTGAACAAGGATTCGCGGTTGGAATGC ATGCTGCTCTTCATATAAACCTTACTATGG	5809
	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCCTTGTTCAAGTACGTGGATTGCTTCTCTAGTCGAATTGCTTC CAGTGTTCATGACTTTGATGCTTCCGC	5810
	AATCCACGTGACTGAAC	5811
	GTTCAAGTACGTGGATT	5812
25 Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT AGAGAAGCAATCCACACGACTGAACAAGGATTCGCGGTTGGAATG CATGCTGCTCTTCATATAAACCTTACTATG	5813
	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTTCAAGTCGTGGATTGCTTCTCTAGTCGAATTGCTTCC AGTGTTCATGACTTTGATGCTTCCGCC	5814

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	CAATCCAC <u>A</u> CGACTGAA	5815
	TTCAGTCG <u>T</u> GTGGATTG	5816
5 Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTATT GGAAATACTGGAA <u>A</u> CAACTCCACCAGGGAAGCAATTCATGCCACT GAGCAGGGTTTTGCTGTTGGAATGCATGC	5817
	GCATGCATTCCAACAGCAAACCCTGCTCAGTGGCATGAATTGCT TCCCTGGTGGAGTTG <u>T</u> TTCCAGTATTTCCAATAACCTTAATTTTCC CACCAAAACAGTTGACTGTATGAGCAATAA	5818
	TACTGGAA <u>A</u> CAACTCCA	5819
	TGGAGTTG <u>T</u> TTCCAGTA	5820
10 Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA GGGAAGCAATTCATG <u>T</u> CACTGAGCAGGGTTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAAACCTTACTATGG	5821
	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA AAACCCTGCTCAGTG <u>A</u> CATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTTCCAATAACCTTAATTTTCCCAC	5822
	AATTCATG <u>T</u> CACTGAGC	5823
	GCTCAGTG <u>A</u> CATGAATT	5824
15 Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC AGGGAAGCAATTCAT <u>A</u> CCACTGAGCAGGGTTTTGCTGTTGGAATG CATGCTGCCCTTCACATAAACCTTACTATG	5825
	CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAA AACCCTGCTCAGTGG <u>T</u> ATGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTTCCAATAACCTTAATTTTCCCACC	5826
	CAATTCAT <u>A</u> CCACTGAG	5827
	CTCAGTGG <u>T</u> ATGAATTG	5828
20 Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC	CTTGCAGGAGACATATTTCAAGATCGTGCTGAGTCAACGTTTTGAG CGGCGAACATTTGCA <u>A</u> ACCCCTTTGAAGTTTATAGAGCACTAAGA GTTGTGAATCCAAGTCCGTATATGGGTTATT	5829
	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATA AACTTCAAAGGGGT <u>T</u> TGCAAATGTTCCGCCGCTCAAACGTTGACT CAGCACGATCTGAAATATGTCTCCTGCAAG	5830
	CATTTGCA <u>A</u> ACCCCTTT	5831
	AAAGGGGT <u>T</u> TGCAAATG	5832
25 Trp Overproduction AS <i>Nicotiana tabacum</i> Asp326Asn GAC-AAC	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA GAAGAACATTTGCT <u>A</u> ACCCATTTGAAGTGTACAGAGCATTAAAGAAT TGTGAATCCAAGCCCATATATGACTTACA	5833

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTAAGTCATATATGGGCTTGGATTGACAATTCTTAATGCTCTGTA CACTTCAAATGGGT <u>T</u> AGCAAATGTTCTTCTCTCAAAGCGTTGACTT AAAACGATTTGAAATATGTCTCCTGCAGC	5834
	CATTTGCT <u>A</u> ACCCATTT	5835
	AAATGGGT <u>T</u> AGCAAATG	5836
5 Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA GGCGTACATTTGCT <u>A</u> ACCCCTTTGAGGTGTACCGTGCATTGCGTA TTGTCAATCCTAGTCCTTATATGGCCTATC	5837
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGGT <u>T</u> AGCAAATGTACGCCTCTCAAACGCTGGC TTAAGACTACTTGAAAAATGTCACCAGCTAG	5838
	CATTTGCT <u>A</u> ACCCCTTT	5839
	AAAGGGGT <u>T</u> AGCAAATG	5840
10 Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA GGCGAACGTTGCA <u>A</u> ACCCATTTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATATATGACTTATT	5841
	AATAAGTCATATATGGGCTTGGATTACAATCCTCAGTGATCTATA GATTTCAAATGGGT <u>T</u> TGCGAACGTTGCGCTTTCAAACGCTGACTT AGTACGATCTGGAATATGTCACCAGCAAG	5842
	CGTTGCA <u>A</u> ACCCATTT	5843
	AAATGGGT <u>T</u> TGCGAACG	5844
15 Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT	CTGGCTGGGGACATATTCCAGCTTGTCTAAGTCAGCGTTTTGAA CGGCGAACATTTGCA <u>A</u> ATCCATTTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT	5845
	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT <u>T</u> TGCAAATGTTGCGCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG	5846
	CATTTGCA <u>A</u> ATCCATTT	5847
	AAATGGAT <u>T</u> TGCAAATG	5848

Example 10**Production of modified starch in plants**

A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α -1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunk* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 20
Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGA AA AGGAACTCGACTCTTTCCTCTCACAAA CGCCGCGCCAAGCCTGCCGTTCTATCGGGG	5849
	CCCCAGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA AAGAGTCGAGTTCTT TT CCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTTTCTCAGTCTCAAGTTC	5850
	GAGGTGGA AA AGGAACT	5851
	AGTTCCT TTT CCACCTC	5852
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA	CAAAACGCCGCGCCAAGCCTGCCGTTCTATCGGGGGAGCCTAT AGGTTGATAGATGTACTAATGAGCAATTGTATTAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	5853
	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTTAA TACAATTGCTCATT AG TACATCTATCAACCTATAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGCGTTTTG	5854
	AGATGTACT A ATGAGCA	5855
	TGCTCATT AG TACATCT	5856
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAT CTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5857
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG ATT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5858
	CTCCAAT AAT CTTGGCT	5859
	AGCCAAG ATT ATTGGAG	5860
Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAC CTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	5861
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG GTT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	5862
	CTCCAAT AAC CTTGGCT	5863
	AGCCAAG GTT ATTGGAG	5864

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCAAAGGAGCTAAACTCTTCCCTCTTACAATGAG AGCCGCAACACCAGCTGTAAATATTCATCTT	5865
	AAGATGAATATTTACAGCTGGTGTTCGGCTCTCATTGTAAGAGG GAAGAGTTTAGCTCCITTTGCCTCCTCCTAGAATGATTGCAGCCAC ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	5866
	GGAGGCAAAGGAGCTAA	5867
	TTAGCTCCITTTGCCTCC	5868
10 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG	CTTGTGTCTTCAAATTATGTTAGGTTCCCTGTTGGTGGATGCTACAG GCTGATCGATATCCITGATGAGTAACTGTATTAACAGCTGCATCAAC AAGATATTTGTGCTGACACAGTTCAACTC	5869
	GAGTTGAACTGTGTCAGCACAAATATCTTGTGATGCAGCTGTTAA TACAGTTACTCATCAGGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTTGAAGACACAAG	5870
	CGATATCCITGATGAGTA	5871
	TACTCATCAGGATATCG	5872
15 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAATATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5873
	GCTGAGAGTTATTATTGTCATAGTGTTCGTACCTCTACGAAACCAC CTCCAAAGTTTATATTATTCCCAAATAAGTTCGTGCTAAATGTCTG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5874
	TGGAATAATATAAACT	5875
	AGTTTATATTATTCCCA	5876
20 Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAACATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	5877
	GCTGAGAGTTATTATTGTCATAGTGTTCGTACCTCTACGAAACCAC CTCCAAAGTTTATGTTATTCCCAAATAAGTTCGTGCTAAATGTCTG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	5878
	TGGAATAACATAAACT	5879
	AGTTTATGTTATTCCCA	5880
25 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGTAAAGGAACCTCGTCTTTTCCCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCCCTATTGGTGG	5881
	CCACCAATAGGAACAGCTGGTTAGCTCTTCTGCTTGTAAAGAGGA AAAAGACGAGTTCCTTTACCACCACCTAGAATGACAGAGGCAACA GCTTTTGGATCTGCCGTTGGTTGTTCTCTCAA	5882
	TGGTGGTAAAGGAACCTC	5883

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTTCCTTTACCACCA	5884
5 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAAACCAGCTGTTCTATTGGTGGTTGTTACC GGCTAATTGATGTACAATGAGTAACTGCATTAAACAGTGGCATAC GGAAAATTTTCATCTTAACACAGTTCAATTC	5885
	GAATTGAACTGTGTTAAGATGAAAATTTCCGTATGCCACTGTAA TGCAGTTACTCATTGTACATCAATTAGCCGGTAACAACCACCAAT AGGAACAGCTGGTTTAGCTCTTCTGCTTG	5886
	TGATGTACAATGAGTA	5887
	TACTCATTGTACATCA	5888
10 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAT	CACAGTTCAATTCCTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAATGTGGGTTTTGGAGATGGATTTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	5889
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5890
	TGGAAATAATGTGGGTT	5891
	AACCCACATTATTTCCA	5892
15 Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAC	CACAGTTCAATTCCTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAACGTGGGTTTTGGAGATGGATTTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	5893
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	5894
	TGGAAATAACGTGGGTT	5895
	AACCCACGTTATTTCCA	5896
20 Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA	ACGTAGATTTGGAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT ACTAGGTGGAGGTAAAGGAACTCGTCTCTTCCCTCTACCAAGC GACGAGCCAAGCCTGCTGTTCCAATTGGAGG	5897
	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGGTGAGAGG GAAGAGACGAGTTCCTTTACCTCCACCTAGTATAATTGCTACAAC GTACTTGGGTCTCTTTTTTCCAAATCTACGT	5898
	TGGAGGTAAGGAACTC	5899
	GAGTTCCTTTACCTCCA	5900

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAAGTGCATCAATAGTGGGATCAA CAAAGTATACATTCTCACTCAATTTAATTC	5901
	GAATTAATTTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGAT GCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAATT GGAACAGCAGGCTTGGCTCGTCGCTTGG	5902
	AGATGTACTAATGAGTA	5903
	TACTCATTAGTACATCT	5904
10 Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAATGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACCTCCAGGGGAGCA	5905
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG	5906
	TGGTACTAATGTCACTT	5907
	AAGTGACATTAGTACCA	5908
15 Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAACGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACCTCCAGGGGAGCA	5909
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG	5910
	TGGTACTAACGTCACTT	5911
	AAGTGACGTTAGTACCA	5912
20 Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA	ATATTGGAGAGGCGTCGGGCAAACCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCGGTAAAGGGACACACCTATTCCCTCTACCAAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	5913
	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCCTTTACCGCCTGGCAGTATGATTGCAGCCACA TTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	5914
	CAGGCGGTAAAGGGACA	5915
	TGTCCCTTTACCGCCTG	5916
25 Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTTGTGCTGACCCAGTTCAATTC	5917
	GAATTGAACTGGGTCAGCACAAAGATCTTGTTAACCCCGCTGTTG ATGCAGTTGCTCATTAGAATGTCGATCAACCTATAGCATCCTCCA GTGGAACAGCAGGGGTTGCAGCTCGATTGG	5918
	CGACATTCTAATGAGCA	5919

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TGCTCATT <u>A</u> GAATGTCG	5920
Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAT</u> GTGAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5921
	GTTTCCCCTTGTTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>ATT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5922
	TGGCAAT <u>AAT</u> GTGAGCT	5923
	AGCTCAC <u>ATT</u> ATTGCCA	5924
Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAC</u> GTGAGCTTCGGAGATGGATTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	5925
	GTTTCCCCTTGTTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>GTT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	5926
	TGGCAAT <u>AAC</u> GTGAGCT	5927
	AGCTCAC <u>GTT</u> ATTGCCA	5928
Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA	CATTCCGGAGGAACCTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCA <u>AA</u> GGGACTCAACTTTTTCTCTCACAAGCA CAAGGGCCACGCCTGCTGTTCTATTGGAGG	5929
	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTTGCTTGTGAGAGG AAAAAGTTGAGTCCCT <u>TTT</u> GCCACCACCCAATATAACAGCAGCAAC CTCATTTGGATCCGCAAAGTTCTCCGGAATG	5930
	TGGTGGCA <u>AA</u> GGGACTC	5931
	GAGTCCCT <u>TTT</u> GCCACCA	5932
Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC	CAAGCACAAGGGCCACGCCTGCTGTTCTATTGGAGGATGCTATA GGCTTATCGATATCCT <u>TC</u> ATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTCATAATGACTCAATTCAACTC	5933
	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGAA ACAGTTGCTCATG <u>AG</u> GATATCGATAAGCCTATAGCATCCTCCAATA GGAACAGCAGGCGTGGCCCTTGTTGCTTG	5934
	CGATATCCT <u>TC</u> ATGAGCA	5935
	TGCTCATG <u>AG</u> GATATCG	5936
Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT <u>AAT</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5937
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>ATT</u> ACCACCAAGGTACGTACGATGAATGTGAC GATTAAGAGATGCTGAGTTGAATTGAGTCA	5938

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGT A ATATCAACT	5939
	AGTTGAT A TTACCACCA	5940
Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT AAC ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	5941
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT G TTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	5942
	TGGTGGT AAC ATCAACT	5943
	AGTTGAT G TTACCACCA	5944
Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGGCGGCA AA GGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCTTATTGGAGG	5945
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCC T TTGCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCGGATCGCTTAATCCTCCTGAAGGAC	5946
	CGGCGGCA AA GGGACTC	5947
	GAGTCCC T TTGCCGCCG	5948
Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCTTATTGGAGGATGTTACA GGCTCATCGACATT C TCATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC	5949
	GAGTTGAACTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG AAGCAGTTGCTCATG A GAATGTCGATGAGCCTGTAAATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	5950
	CGACATT C TCATGAGCA	5951
	TGCTCATG A GAATGTCG	5952
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AAT ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5953
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT ATT CCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAAGTGGGTCA	5954
	CGGCGGG AAT ATCAATT	5955
	AATTGAT ATT CCCCGCCG	5956
Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AAC ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5957

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGATGTTCCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	5958
	CGGCGGGAAACATCAATT	5959
	AATTGATGTTCCCCGCCG	5960
Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCCAAAGGAGTTCAACTCTTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTTGGAGG	5961
	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTGAGAGG AAAGAGTTGAACTCCTTTGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	5962
	TGGAGGCCAAAGGAGTTC	5963
	GAACTCCTTTGCCTCCA	5964
Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT	CAAGCACAAAGGGCTACCCCCGCTGTTCTGTTGGAGGATGTTACA GGCTTATTGACATCCTTATGAGCAATTGCTTCAATAGCGGAATAAA TAAATATTTGTGATGACTCAGTTCAATTC	5965
	GAATTGAACTGAGTCATCACAAATATTTTATTATTCCGCTATTGAA GCAATTGCTCATAAGGATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGTGCTTG	5966
	TGACATCCTTATGAGCA	5967
	TGCTCATAAGGATGTCA	5968
Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGGAATATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5969
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGATATTCCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5970
	TGGTGGGAATATCAACT	5971
	AGTTGATATTCCCACCA	5972
Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAC	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATAC ATACCTTGGTGGGAACATCAACTTTACTGATGGGTCTGTGCAGGT ATTGGCTGCTACACAAATGCCTGACGAACC	5973
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGATGTTCCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	5974
	TGGTGGGAACATCAACT	5975
	AGTTGATGTTCCCACCA	5976

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCA AA GGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG	5977
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCCT TTT GCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCCGTAATTCCTGCGGAAGG	5978
	CGGTGGCA AA GGGACTC	5979
	GAGTCCCT TTT GCCACCG	5980
10 Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGATATTCTCATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC	5981
	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATG AGA ATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	5982
	CGATATTCTCATGAGCA	5983
	TGCTCATG AGA ATATCG	5984
15 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AAT ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5985
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT ATT CCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5986
	CGGCGGG AAT ATCAATT	5987
	AATTGAT ATT CCCCGCCG	5988
20 Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG AAC ATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	5989
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT GTT CCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	5990
	CGGCGGG AAC ATCAATT	5991
	AATTGAT GTT CCCCGCCG	5992
25 Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGT AA GGGACTCAGCTTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCTATTGGAGG	5993
	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCCT TTT ACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG	5994
	TGGTGGT AA GGGACTC	5995

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GAGTCCCTTTACCACCA	5996
5 Increased Starch ADPGPP <i>Zea mays</i> Pro124Leu CCC-CTC	CAAGCACAAAGGGCCACCCCTGCTGTTCTATTGGAGGATGTTACA GGCTTATTGATATCCTCATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTTGTTATGACTCAGTTCAACTC	5997
	GAGTTGAACTGAGTCATAACAAATATCTTGTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGGTGGCCCTTGTGCTTG	5998
	TGATATCCTCATGAGCA	5999
	TGCTCATGAGGATATCA	6000
10 Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAATATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6001
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATATTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6002
	TGGTGGGAATATCAACT	6003
	AGTTGATATTCCCACCA	6004
15 Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAACATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	6005
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATGTTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	6006
	TGGTGGGAACATCAACT	6007
	AGTTGATGTTCCCACCA	6008
20 Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG	CTTGAGAGGCCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGGAAGGGAACTCGTCTTTTCCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	6009
	CTCCCATTTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG AAAAGACGAGTTCCCTTTCCCCCTCCTAGAATGATTGCTACTACTG TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	6010
	GAGGGGGAAGGGAACT	6011
	AGTTCCCITCCCCCTC	6012
25 Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA	CCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC	6013
	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTTGG	6014

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTACT <u>A</u> ATGAGCA	6015
	TGCTCATT <u>A</u> GTACATCA	6016
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAT</u> GTGCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6017
	AATTCACCTGGTGTGTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>ATT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG	6018
	TGGCAAT <u>AAT</u> GTGCACAT	6019
	ATGTGAC <u>ATT</u> ATTGCCA	6020
Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAC</u> GTGCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	6021
	AATTCACCTGGTGTGTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>GTT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG	6022
	TGGCAAT <u>AAC</u> GTGCACAT	6023
	ATGTGAC <u>GTT</u> ATTGCCA	6024
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAAG</u> GGGACTCGCCTCTTTCCTCTTACTAGCA GGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6025
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>TTT</u> ACCACCACCCAGCACAATTGCAGCCACA TTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6026
	TGGTGGT <u>AAAG</u> GGGACTC	6027
	GAGTCCC <u>TTT</u> ACCACCA	6028
Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAC</u> GGGACTCGCCTCTTTCCTCTTACTAGCA GGAGAGCTAAGCCAGCAGTGCCAATTGGAGG	6029
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>GTT</u> ACCACCACCCAGCACAATTGCAGCCAC ATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	6030
	TGGTGGT <u>AAC</u> GGGACTC	6031
	GAGTCCC <u>GTT</u> ACCACCA	6032
Increased Starch ADPGPP <i>Beta vulgaris</i> Pro126Leu CCT-CTT	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTTAC AGGCTGATTGATGTGCTTATGAGCAACTGCATCAACAGTGGCATT AGAAAGATTTTCATTCTTACCCAGTTCAATTC	6033

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Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGAACTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA TGCAGTTGCTCATAAGCACATCAATCAGCCTGTAACACCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	6034
	TGATGTGCITATGAGCA	6035
	TGCTCATAAGCACATCA	6036
Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAATGTGAATTTGGGGATGGCTTTGTGGAGGT TTTGCTGCTACACAAACACCTGGAGAATC	6037
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTACATTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6038
	TGGAGATAATGTGAATT	6039
	AATTCACATTATCTCCA	6040
Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAACGTGAATTTGGGGATGGCTTTGTGGAGGT TTTTGCTGCTACACAAACACCTGGAGAATC	6041
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTACGTTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	6042
	TGGAGATAACGTGAATT	6043
	AATTCACGTTATCTCCA	6044

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Table 21
Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 10 Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTC TTCTAACTTTGTGTGAAGAACTTCACCTTTTCAACAATCATGGTGCTT CTTCATGCTCTGATGTCGCTCAGATTAC	6045
	GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTGA AAAGTGAAGTTCTTCACACAAAGTTAGAAGAAGCAGTCACAGTTGC CATTATGAACTACCCGTTTACCTGGATTC	6046
	CTTTGTGTGAAGAACTT	6047
	AAGTTCTTCACACAAAG	6048
15 Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTT CTAACTTTGTGTCAAGAAGTTCACCTTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	6049
	AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTT GAAAAGTGAAGTTCAATGACACAAAGTTAGAAGAAGCAGTCACAGTT GCCATTATGAACTACCCGTTTACCTGGAT	6050
	TTGTGTCAAGAAGTTC	6051
	TGAAGTTCAATGACACAA	6052
20 Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA	TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTT TGTGTCAAGAAGTTCACCTTTTCAACAATCATGGTGCTTCTTCTATGCT CTGATGTCGCTCAGATTACCTTAAAAGG	6053
	CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCAT GATTGTTGAAAAGTCAAGTTCTTGACACAAAGTTAGAAGAAGCAGT CACAGTTGCCATTATGAACTACCCGTTTA	6054
	AAGAAGTTCACCTTTTCA	6055
	TGAAAAGTCAAGTTCTT	6056
25 Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA	TGACTGCTTCTTCTAACTTTGTGTCAAGAAGTTCACCTTTTCAACAAT CATGGTGCTTCTTGATGCTCTGATGTCGCTCAGATTACCTTAAAAG GCCAATCCTTGACTCATTGTGGGTTAAG	6057
	CTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAG CGACATCAGAGCATCAAGAAGCACCATGATTGTTGAAAAGTGAAGT TCTTGACACAAAGTTAGAAGAAGCAGTCA	6058
	TGCTTCTTGATGCTCTG	6059
	CAGAGCATCAAGAAGCA	6060

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA	TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATG GTGCTTCTTCATGATCTGATGTCGCTCAGATTACCTTAAAAGGCCA ATCCTTGACTCATTGTGGGTAAAGGTCA	6061
	TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATGATTGTTGAAAAGTG AAGTTCTTGACACAAAGTTAGAAGAAGCA	6062
	TCTTCATGATCTGATGT	6063
	ACATCAGATCATGAAGA	6064
10 Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTTAAACAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCCTCACAATGGGTTGAGAT	6065
	ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCT GGGCCAAGTTTGTAAAGTATCCGGTGAAGACGTTGCTCCACCAT GGACATGTGACACCAACTGTGAAGCTGTTAC	6066
	CGGATACTTAAACAAAC	6067
	GTTTGTAAAGTATCCG	6068
15 Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG	CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAAACAACTAGGCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	6069
	ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGA GGCCAACCTGGGCCAGTTTGTAAAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	6070
	AACAACTAGGCCAGG	6071
	CCTGGGCCAGTTTGT	6072
20 Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG	TTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAACTTGGCCTAGGTTGGCCTCAGGAACCAGCAATTCCT CACAATGGGTTGAGATCAATAAACATGGTTG	6073
	CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCTAGGCCAAGTTTGTAAAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	6074
	ACTTGGCCTAGGTTGGC	6075
	GCCAACCTAGGCCAAGT	6076
25 Waxy starch GBSS <i>Antirrhinum majus</i> Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAAACAACTTGGCCCAG GTTGGCCTCAGGAACAGCAATTCCTCACAATGGGTTGAGATCAA TAAACATGGTTGATAAGCTTCAAATGAGGA	6077
	TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTG TGAGTGAATTGCTAGTTCTGAGGCCAACCTGGGCCAAGTTTGT TTAGTATCCGGTGAAGACGTTGCTCCACC	6078

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCAGGAAC <u>T</u> AGCAATTC	6079
	GAATTGCTA <u>G</u> TTCCTGA	6080
5 Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA	GGAGCAACGTCTTCACCGGATACTAAAACAACTTGGCCCAGGTT GGCCTCAGGAACCAGT <u>A</u> ATTCCTCACAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTTCAAATGAGGAACA	6081
	TGTTCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCA TTGTGAGTGAATT <u>A</u> CTGGTTCCTGAGGCCAACCTGGGCCAAGTTT GTTTATGATATCCGGTGAAGACGTTGCTCC	6082
	GGAACCAGT <u>A</u> ATTCCT	6083
	AGTGAATT <u>A</u> CTGGTTC	6084
10 Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTG GGGGTGCCACTTCTT <u>G</u> GAGAATCAAAAGTGGGGTTGGGTCAATTAG CCCTGAGGAGCCAAGCTGTGACTCACAATG	6085
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACC CCACTTTTGATTCTC <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	6086
	CCACTTCTT <u>G</u> GAGAATCA	6087
	TGATTCTC <u>A</u> AGAAGTGG	6088
15 Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGG GTGCCACTTCTGGAT <u>A</u> AATCAAAAGTGGGGTTGGGTCAATTAGCCC TGAGGAGCCAAGCTGTGACTCACAATGGGT	6089
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCA ACCCCACTTTTGATT <u>A</u> TCCAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	6090
	CTTCTGGAT <u>A</u> AATCAAAA	6091
	TTTTGATT <u>A</u> TCCAGAAG	6092
20 Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGC CACTTCTGGAGAAT <u>G</u> AAAAAGTGGGGTTGGGTCAATTAGCCCTGAG GAGCCAAGCTGTGACTCACAATGGGTGAG	6093
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGA CCCAACCCCACTTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACA TGAGAAACAAAGTGTGAGGCAGTTATAGTCG	6094
	TGGAGAAT <u>G</u> AAAAAGTGG	6095
	CCACTTTT <u>C</u> ATTCTCCA	6096

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCA CTTCTGGAGAATCA <u>T</u> AAGTGGGGTTGGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC	6097
	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT GACCCAACCCCACTT <u>A</u> TGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTATAGT	6098
	GAGAATCA <u>T</u> AAGTGGGG	6099
	CCCCACTT <u>A</u> TGATTCTC	6100
10 Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG	CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGGT <u>A</u> GGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA	6101
	TTGTTACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCA GGGCTAATTGACCC <u>T</u> ACCCCACTTTTGATTCTCCAGAAGTGGCAC CCCCACAGACATGAGAAACAAAGTGTGAGG	6102
	AGTGGGGT <u>A</u> GGGTCAAT	6103
	ATTGACCC <u>T</u> ACCCCACT	6104
15 Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG	CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAAC GGTGACGGGGTCTTAG <u>G</u> GTGGTGTGAGAAAGCGCGTGCTTCAATTC CCAGGGAAGAACAGAAGCCAAAGTGAATTCA	6105
	TGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCAC <u>C</u> TAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATCGCCGATG	6106
	GGGTCTTAG <u>G</u> GTGGTGTC	6107
	GACACCAC <u>C</u> TAAGACCC	6108
20 Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG	ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGG GGTCTTATGTGGTGT <u>A</u> GAGAAGCGCGTGCTTCAATTCCCAGGGAA GAACAGAAGCCAAAGTGAATTCACCTCAGAA	6109
	TTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGA AGCACGCGCTTCTC <u>T</u> ACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	6110
	TGTGGTGT <u>A</u> GAGAAGCG	6111
	CGCTTCTC <u>T</u> ACACCACA	6112

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGTCTGTAAGCGCGTGCTTCAATTCAGGGAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	6113
	TCTTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATT GAAGCACGCGCTTCACGACACCACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	6114
	TGGTGTCTGTAAGCGCG	6115
	CGCGCTTCACGACACCA	6116
10 Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA	ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGTGATTCAATTCAGGGAAGAACAGAAGCCAA AGTGAATTCACCTCAGAAGATAAATCTCAAT	6117
	ATTGAGATTTATCTTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTC CCTGGGAATTGAATCACGCGCTTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	6118
	AGCGCGTGATTCAATTC	6119
	GAATTGAATCACGCGCT	6120
15 Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTGCGAGAAGC GCGTGCTTCAATTCCTAGGGAAGAACAGAAGCCAAAGTGAATTCA CCTCAGAAGATAAATCTCAATAGCCAAGCAT	6121
	ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACCTTTGGCT TCTGTTCTTCCCTAGGAATTGAAGCACGCGCTTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG	6122
	TCAATTCCTAGGGAAGA	6123
	TCTTCCCTAGGAATTGA	6124
20 Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGC AAGCATCACAGCTTGACACCACTTTGTGTCAAGAAGCCAACTTCA CTAGACACCAAATCAACCTTGTCACAGAT	6125
	ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTG ACACAAAGTGGTGTCAAGCTGTGATGCTTGCCATGTGATGTGTGG TCTACAAAAGGGGAATCTACCAAGCTACA	6126
	CACAGCTTGACACCACT	6127
	AGTGGTGTCAAGCTGTG	6128
25 Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA	TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTTGTGTGAAGAAGCCAACTTCACTAGACACCAAATCA ACCTTGTCACAGATAGGACTCAGGAACCA	6129
	TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTG AAGTTTGGCTTCTTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGTGGTCTACAAAAGGGGA	6130

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGTGAAGAAGCC	6131
	GGCTTCTTCACACAAAG	6132
Waxy starch GBSS <i>Solanum tuberosum</i> Arg13Term AGA-TGA	CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGTCAAGAAGCCAACTTCACTAGACACCAAATCAAC CTTGTCACAGATAGGACTCAGGAACCATA	6133
	TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAG TGAAGTTTGGCTTCATGACACAAAGTGGTGTGAAGCTGTGATGCTT GCCATGTGATGTGTGGTCTACAAAAGGG	6134
	TTGTGTCAAGAAGCCAA	6135
	TTGGCTTCATGACACAA	6136
Waxy starch GBSS <i>Solanum tuberosum</i> Gln15Term CAA-TAA	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGTCAAGAAGCTAAACTTCACTAGACACCAAATCAACCTTGTC ACAGATAGGACTCAGGAACCATACTCTGA	6137
	TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGT GTCTAGTGAAGTTTAGCTTCTTGACACAAAGTGGTGTGAAGCTGTG ATGCTTGCCATGTGATGTGTGGTCTACAA	6138
	CAAGAAGCTAAACTTCA	6139
	TGAAGTTTAGCTTCTTG	6140
Waxy starch GBSS <i>Solanum tuberosum</i> Ser17Term TCA-TGA	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTC AAGAAGCCAACTTGACTAGACACCAAATCAACCTTGTCACAGATA GGACTCAGGAACCATACTCTGACTCACAA	6141
	TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTG ATTTGGTGTCTAGTCAAGTTTGGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTTGCCATGTGATGTGTGG	6142
	CCAACTTGACTAGACA	6143
	TGTCTAGTCAAGTTTGG	6144
Waxy starch GBSS <i>Pisum sativum</i> Gly6Term GGA-TGA	GTCGATCACTCTTCTCTACCGCCGAAACAGATTTTGACACAAAA TGGCAACAATAACGTGATCTTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA	6145
	TAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGT CGGCATTGAAGATCACGTTATTGTTGCCATTTTTGTGTCAAATCT GTTTCGGCGGTGAGAGAAGAGTGATCGAC	6146
	CAATAACGTGATCTTCA	6147
	TGAAGATCACGTTATTG	6148

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAAC AATAACGGGATCTTGAATGCCGACGAGAACC GCGTGCTTCAATTA CCAAGGAAGATCAGCAGAGTCTAAACTGAA	6149
	TTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGG TTCTCGTCGGCATTCAAGATCCCGTTATTGTTGCCATTTTGTGTC AAAATCTGTTTCGGCGGTGAGAGAAGAGT	6150
	GGGATCTTGAATGCCGA	6151
	TCGGCATTCAAGATCCC	6152
10 Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA	ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGAT CTTCAATGCCGACGTGAACCGCGTGCTTCAATTACCAAGGAAGAT CAGCAGAGTCTAAACTGAATTTGCCTCAGA	6153
	TCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATT GAAGCACGCGGTTCAAGTCGGCATTGAAGATCCCGTTATTGTTGC CATTTTGTGTCAAATCTGTTTCGGCGGT	6154
	TGCCGACGTGAACCGCG	6155
	CGCGGTTCAAGTCGGCA	6156
15 Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA	AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCG ACGAGAACC GCGTGAATTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATTTGCCTCAGATACACTTCAAT	6157
	ATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTT CCTTGGTAATTGAATCAGCGGTTCTCGTCGGCATTGAAGATCCC GTTATTGTTGCCATTTTGTGTCAAATCT	6158
	ACCGCGTGAATTCAATTA	6159
	TAATTGAATCAGCGGT	6160
20 Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG	CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAAC CGCGTGCTTCAATTAGCAAGGAAGATCAGCAGAGTCTAAACTGAAT TTGCCTCAGATACACTTCAATAACAACCAA	6161
	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTG CTGATCTTCCTTGCTAATTGAAGCACGCGGTTCTCGTCGGCATTGA AGATCCCGTTATTGTTGCCATTTTGTG	6162
	TTCAATTAGCAAGGAAG	6163
	CTTCCTTGCTAATTGAA	6164
25 Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA	TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTTCCAGGAGCTGACACTTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTTGTCTCACACTGGACCCTG	6165
	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCAT GGATGCTCAAGTGTGAGCTCCTGGAAACGAAATGTGCAGCTATTA CAGTTGCCATGGTGCTCTCTCCGGTGTAGA	6166

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	CAGGAGCTGACACTTGA	6167
	TCAAGTGTGAGCTCCTG	6168
	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCTGTTT CCAGGAGCTCACACTAGAGCATCCATGCATTAGAGACTAAGGCTA ATAATTTGTCTCACACTGGACCCTGGACCCA	6169
	TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCTCTAGTGTGAGCTCCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGTCTCTCTCCGG	6170
	CTCACACTAGAGCATCC	6171
10	GGATGCTCTAGTGTGAG	6172
	TGGCAACTGTAATAGCTGCACATTTCTGTTTCCAGGAGCTCACACTT GAGCATCCATGCATGAGAGACTAAGGCTAATAATTTGTCTCACACT GGACCCTGGACCCAACTATCACTCCCAA	6173
	TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTA TTAGCCTTAGTCTCTCATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA	6174
	CCATGCATGAGAGACTA	6175
	TAGTCTCTCATGCATGG	6176
15	GCAACTGTAATAGCTGCACATTTCTGTTTCCAGGAGCTCACACTTGA GCATCCATGCATTATAGACTAAGGCTAATAATTTGTCTCACACTGG ACCCTGGACCCAACTATCACTCCCAATG	6177
	CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCTATAATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC	6178
	ATGCATTATAGACTAAG	6179
	CTTAGTCTATAATGCAT	6180
20	GTAATAGCTGCACATTTCTGTTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACTTAGGCTAATAATTTGTCTCACACTGGACCCTG GACCCAACTATCACTCCCAATGGTTAA	6181
	TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCTAAGTCTCTAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC	6182
	TAGAGACTTAGGCTAAT	6183
	ATTAGCCTAAGTCTCTA	6184

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA	ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGCGTGGCGTGAAAAGGCGCGTGGAGTACAGAGACAAAA GTGAAATCTTCGGGTCAGATGAGCCTGAACCG	6185
	CGGTTCAAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTAC TCCACGCGCCTTTTACAGCCACGCACGATGCCATCGATACCGTTG CCATGCTTATACCGGTGACGGAGGAGTTGT	6186
	CGTGGCGTGAAAAGGCG	6187
	CGCCTTTTACAGCCACG	6188
10 Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGC GTCAAAGGCGCGTGAAAGTACAGAGACAAAAGTGAAATCTTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA	6189
	TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACT TTTGTCTCTGTACTTCACGCGCCTTTTGACGCCACGCACGATGCC ATCGATACCGTTGCCATGCTTATACCGGTG	6190
	GGCGCGTGAAAGTACAGA	6191
	TCTGTACTTCACGCGCC	6192
15 Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG	ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAA GGCGCGTGGAGTACATAGACAAAAGTGAAATCTTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG	6193
	CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGA TTTCACTTTTGTCTATGTACTCCACGCGCCTTTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT	6194
	GGAGTACATAGACAAA	6195
	TTTTGTCTATGTACTCC	6196
20 Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys21Term AAA-TAA	ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGC GTGGAGTACAGAGACATAAGTGAAATCTTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTTGA	6197
	TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACC CGAAGATTTCACTTATGTCTCTGTACTCCACGCGCCTTTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT	6198
	CAGAGACATAAGTGAAA	6199
	TTTCACTTATGTCTCTG	6200
25 Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys23Term AAA-TAA	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAG TACAGAGACAAAAGTGTAATCTTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTTGAGATCTC	6201
	GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCAT CTGACCCGAAGATTACACTTTTGTCTCTGTACTCCACGCGCCTTTT GACGCCACGCACGATGCCATCGATACCGT	6202

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAAAAGTGTAATCTTCG	6203
	CGAAGATTACACTTTTG	6204
5 Waxy starch GBSS <i>Triticum aestivum</i> Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG GTTCCATTCTAATTAGTGTTCTTATCAAACAAACAGTGTTGGTTCA CTGAAACTGTGCGCTCACATCCAATTCCAG	6205
	CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTTT GTTTGATAAGAACACTAATTAGGAATGGAACCCATTGGTGCAGCCT CTCAATGACGACCTTTTCGAGCTAGGCGC	6206
	CCTAATTAGTGTTCTTA	6207
	TAAGAACACTAATTAGG	6208
10 Waxy starch GBSS <i>Triticum aestivum</i> Cys8Term TGT-TGA	CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTT CATTCTAATTATTGATCTTATCAAACAAACAGTGTTGGTTCACTGA AACTGTGCGCTCACATCCAATTCCAGCAA	6209
	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTTGATAAGATCAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTTCGAGCTAGG	6210
	AATTATTGATCTTATCA	6211
	TGATAAGATCAATAATT	6212
15 Waxy starch GBSS <i>Triticum aestivum</i> Tyr10Term TAT-TAG	TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTAGCAAACAAACAGTGTTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	6213
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTTGTTTGCTAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCGA	6214
	TGTTCTTAGCAAACAAA	6215
	TTTGTTTGCTAAGAACA	6216
20 Waxy starch GBSS <i>Triticum aestivum</i> Gln11Term CAA-TAA	CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCTT AATTATTGTTCTTATTAAACAAACAGTGTTGGTTCACTGAAACTGTC GCCTCACATCCAATTCCAGCAATCTTGTA	6217
	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTTGTTTAATAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCG	6218
	GTTCTTATTAAACAAAC	6219
	GTTTGTTTAATAAGAAC	6220

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTTGACTGAAACTGTGCGCTCACATCCAATTCCAGC AATCTTGTAACAATGAAGTTATGTTCT	6221
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGTCAACCAACACTGTTTGTGATAAGAACAATA ATTAGGAATGGAACCCATTGGTGCAGCCT	6222
	TGTTGGTTGACTGAAAC	6223
	GTTTCAGTCAACCAACA	6224
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCCTCCTCGGCATCACCGACAGGTT CCGGCGTGACAGTTTCTAGGGCGTGAGGCCCGGAGCCCGGCG GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	6225
	TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCCGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6226
	CAGGTTTCTAGGGCGTG	6227
	CACGCCCTAGAAACCTG	6228
15 Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCGGAGCCCGGCGGATGCGGCTC TCGGCATGAGGACCGTCTAGAGCTAGCGCCGCCCAACGCAAAGC CGGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	6229
	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCGGCTTTGCGTT GGGGCGGCGCTAGCTCAGACGGTCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6230
	GGACCGTCTAGAGCTAGC	6231
	GCTAGCTCAGACGGTCC	6232
20 Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAG CTAGCGCCGCCCAACGTAAAGCCGGAAGCGCACCGCGGGACC CGGCGGTGCCTCTCCATGGTGGTGCGGCCACCG	6233
	CGGTGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	6234
	CCCCAACGTAAAGCCGG	6235
	CCGGCTTTACGTTGGGG	6236
25 Waxy starch GBSS <i>Triticum aestivum</i> Lys56Term AAA-TAA	GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCG CCCCAACGCAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTG CCTCTCCATGGTGGTGCGGCCACCGGCAGCGGCG	6237
	CGCCGCTGCCGGTGCGCGCACCAACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAG CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC	6238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	AAAGCCGGT <u>A</u> AGCGCAC	6239
	GTGCGCTT <u>A</u> CCGGCTTT	6240
5 Waxy starch GBSS <i>Triticum aestivum</i> Glu85Term GAG-TAG	CTCTCCATGGTGGTGC GCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCTGTCGGCGCC <u>T</u> AGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCTCTCGGGGGCCTCCCCCAG	6241
	CTGGGGGGAGGCCCGAGGACGTGCGCGAGGCCGCGGTCTT GCTCCAGGGCGCCATCT <u>A</u> GGCGCCGACGAACACGAGGTTTCATGC CGCCGCTGCCGGTGGCGCGCACCAACCATGGAGAG	6242
	TCGGCGCC <u>T</u> AGATGGCG	6243
	CGCCATCT <u>A</u> GGCGCCGA	6244
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCTG <u>T</u> AGCTCGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTTTC	6245
	GAAAACCTGCACGCCGGAACCTGTGCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> CGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	6246
	TCACGTCTG <u>T</u> AGCTCGCC	6247
	GGCGAGCT <u>A</u> CGACGTGA	6248
15 Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCTCTCGGCATCACCGACAGGTT CCGGCGTGCAGTTTTT <u>T</u> AGGGTGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6249
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCT <u>A</u> AAAACTGCACGCCGGAACCTGTCCGT GATGCCGAGGACGGTGCCGAGGTGGCGAGCTG	6250
	CAGGTTTTT <u>T</u> AGGGTGTG	6251
	CACACCCT <u>A</u> AAAACTG	6252
20 Waxy starch GBSS <i>Triticum aestivum</i> Lys52Term AAG-TAG	CCCCGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCG <u>T</u> AGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGC GCG	6253
	CGCGCACCAACATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCT <u>A</u> CGGGGCGGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6254
	CCGCCCCG <u>T</u> AGCAACAA	6255
	TTGTTGCT <u>A</u> CGGGGCGG	6256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGGAAGTAACAAAGCCGGAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6257
	TGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6258
	CCCCGAAGTAACAAAGC	6259
	GCTTTGTTACTTCGGGG	6260
10 Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGGAAGCAATAAAGCCGGAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6261
	CCGTGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6262
	CGAAGCAATAAAGCCGG	6263
	CCGGCTTTATTGCTTCG	6264
15 Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAAGTTTCTAGGGCGTGAGGCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	6265
	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCCGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6266
	CAGGTTTCTAGGGCGTG	6267
	CACGCCCTAGAAACCTG	6268
20 Waxy starch GBSS <i>Triticum durum</i> Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCGTAGCAAAGCCGGAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	6269
	TGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTCGCTCCGATAGTCC TCATGACGAGGGCCGCATCCGCCGGGTTCCGGGG	6270
	CCGCCCCGTAGCAAAGC	6271
	GCTTTGCTACGGGGCGG	6272
25 Waxy starch GBSS <i>Triticum durum</i> Gln53Term CAA-TAA	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCGGAAGTAAGCCGGAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	6273
	CCGTGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACTTCGGGGCGGCGCTCGCTCCGATAG TCCTCATGACGAGGGCCGCATCCGCCGGGTTCCG	6274

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAGTAAAGCCGG	6275
	CCGGCTTTACTTCGGGG	6276
Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGGTAAGCGCACCGCGGGAGCCGGCGGTGC CTCTCCATGGTGGTGC GCGCCACGGGCAGCGGCG	6277
	CGCCGCTGCCCCTGGCGCGCACCAACCATGGAGAGGCACCGCCG GCTCCCGCGGTGCGCTTACCGGCTTTGCTTCGGGGCGGCGCTCG CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	6278
	AAAGCCGGTAAGCGCAC	6279
	GTGCGCTTACCGGCTTT	6280
Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCACCC GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGC GCGCCACGGG CAGCGGCGGCATGAACCTCGTGTTCTGTCGGCGCC	6281
	GGCGCCGACGAACACGAGGTTTCATGCCGCCGCTGCCCGTGGCG CGCACCACCATGGAGAGTCACCGCCGGCTCCCGCGGTGCGCTTT CCGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	6282
	CGGCGGTGACTCTCCAT	6283
	ATGGAGAGTCACCGCCG	6284
Waxy starch GBSS <i>Triticum turgidum</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTG CAGGTTTTTAGGGTGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	6285
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6286
	CAGGTTTTTAGGGTGTG	6287
	CACACCCTAAAAACCTG	6288
Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCG GAGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCCATGGTGGTGC GCG	6289
	CGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6290
	CCGCCCGTAGCAACAA	6291
	TTGTTGCTACGGGGCGG	6292

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA	CGGAGCCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGCAAGTAACAAAGCCGGAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGC GCGCCA	6293
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAG TCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6294
	CCCCGAAGTAACAAAGC	6295
	GCTTTGTTACTTCGGGG	6296
10 Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGA GCGCCGCCCGCAAGCAATAAGCCGGAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCCATGGTGGTGC GCGCCACGG	6297
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGG TAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6298
	CGAAGCAATAAGCCGG	6299
	CCGGCTTTATTGCTTCG	6300
15 Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCC CGAAGCAACAAAGCCGGTAAGCGCACCGCGGACCCGGCGGTG CCTCTCCATGGTGGTGC GCGCCACGGGCAGCGCCG	6301
	CGGCGCTGCCCGTGCGCGCACCAACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGTTGCTTCGGGGCGGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	6302
	AAAGCCGGTAAGCGCAC	6303
	GTGCGCTTACCGGCTTT	6304
20 Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGTT CCGCCATGCAGTTTTCTAGGGCGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	6305
	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCATGGCGGAACCTGTCGGT GATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	6306
	CAGGTTTC TAGGGCGTG	6307
	CACGCCCTAGAAACCTG	6308
25 Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCGGAGCCCGGCAGATGCGCCGC TCGGCATGAGGACTGTCTGAGCGAGCGCCGCCCGCAAGCAACAA AGCCGGAAGCGCACCGCGGGACCCGGCGGTGCC	6309
	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTC GGGGCGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGGCGCAT CTGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	6310

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGA <u>CT</u> GTCTGAGCGAGC	6311
	GCTCGCTCAGACAGTCC	6312
Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCTG GAGCGAGCGCCGCCCGCTAGCAACAAAGCCGAAAGCGCACCG CGGGACCCGGCGGTGCCTCTCGATGGTGGTGC	6313
	CGCGCACCAACATCGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGACAGTCC TCATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	6314
	CCGCCCGTAGCAACAA	6315
	TTGTTGCTACGGGGCGG	6316
Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCTGGAG CGAGCGCCGCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGC	6317
	TGGCGCGCACCAACATCGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGACAG TCCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	6318
	CCCCGAAGTAACAAAGC	6319
	GCTTTGTTACTTCGGGG	6320
Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCTGGAGCGA GCGCCGCCCGAAGCAATAAAGCCGAAAGCGCACCGCGGGAC CCGGCGGTGCCTCTCGATGGTGGTGC	6321
	CGGTGGCGCGCACCAACATCGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGA CAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	6322
	CGAAGCAATAAAGCCGG	6323
	CCGGCTTTATTGCTTCG	6324
Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCTG GCTCTCACCACGTCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTGCGCGCGTCTGCTGCTGC	6325
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	6326
	CCACGTCTAGCTCGCC	6327
	GGCGAGCTAGGACGTGG	6328

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGGT	6329
	AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	6330
	CGCCACCTAGGCCACCG	6331
	CGGTGGCCTAGGTGGCG	6332
10 Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGTAGGCCCGCTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	6333
	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCTACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6334
	TGACAGGTAGGCCCGCT	6335
	ACGGCGCCTACCTGTCA	6336
15 Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTGGCGCCGTAGTCGCTGCTCCGCCACGGGTTCCAGG GCCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	6337
	GCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGACTACGGCGCCGACCTGTCAGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6338
	GGCGCCGTAGTCGCTGC	6339
	GCAGCGACTACGGCGCC	6340
20 Waxy starch GBSS <i>Oryza glaberrima</i> Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	6341
	GTCGCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGCTACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6342
	GCCGTCGTAGCTGCTCC	6343
	GGAGCAGCTACGACGGC	6344
25 Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG	TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTG GCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTGGCGCCGTCGTCGCTGC	6345
	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTAGCTCTTGCTGTGGA	6346

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACGTCCTAGCTCGCC	6347
	GGCGAGCTAGGACGTGG	6348
Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG	CTAAACAGCCGACCGTGTGCACCACCATGTCGGTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCCGACAGG TCGGCGCCGTCGTCGCTGCTTCGCCACGGGTT	6349
	AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCGGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	6350
	CGCCACCTAGGCCACCG	6351
	CGGTGGCCTAGGTGGCG	6352
Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCCGACAGGTAGGCGCCGTCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	6353
	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA GCAGCGACGACGGCGCCTACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	6354
	CGACAGGTAGGCGCCGT	6355
	ACGGCGCCTACCTGTCTG	6356
Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC GACAGGTGGCGCCGTAGTCGCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGC	6357
	GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACC CGTGGCGAAGCAGCGACTACGGCGCCGACCTGTCGGCGATGCC GAAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	6358
	GGCGCCGTAGTCGCTGC	6359
	GCAGCGACTACGGCGCC	6360
Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC AGGTGGCGCCGTCGTAGCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCCAGCCGGCGGGGACGCATC	6361
	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCCGTGGCGAAGCAGCTACGACGGCGCCGACCTGTCGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	6362
	GCCGTCGTAGCTGCTTC	6363
	GAAGCAGCTACGACGGC	6364

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC GGCTCTGGCCACGTCTTAGCTCGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTTT	6365
	GAAAACCTGGACGCCGGAATCTGTGCGGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCGCCATGGCGC CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	6366
	CCACGTCTTAGCTCGCC	6367
	GGCGAGCTAGGACGTGG	6368
10 Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGT CCTCGGCGTCACCGACTGATTCCGGCGTCCAGGTTTTTCAAGGCCT CAGGCCCGGAACCCGGCGGATGCGGCGCTTG	6369
	CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATCAGTTCGGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	6370
	TCACCGACTGATTCCGG	6371
	CCGGAATCAGTTCGGTGA	6372
15 Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCTCCTCGGCGTCACCGACAGATT CCGGCGTCCAGGTTTTTAGGGCCTCAGGCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	6373
	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCTAAAAACCTGGACGCCGGAATCTGTGCGTG ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	6374
	CAGGTTTTTAGGGCCTC	6375
	GAGGCCCTAAAAACCTG	6376
20 Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA	GGTTTTTAGGGCCTCAGGCCCGGAACCCGGCGGATGCGGCGCT TGGTATGAGGACTATCTAGCAAGCGCCGCCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	6377
	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTCCGGCTTTGCTTC GGGGCGGCGCTTGCTCAGATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	6378
	GGACTATCTAGCAAGC	6379
	GCTTGCTCAGATAGTCC	6380
25 Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCGTAGCAAAGCCGGAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA	6381
	TGGCGCTCACCACCACGGAGAGGCACCGCCGGCTCCCGCGGTG CGCTTCCGGCTTTGCTACGGGGCGGCGCTTGCTCCGATAGTCC TCATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	6382

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGCCCCG <u>T</u> AGCAAAGC	6383
	GCTTTGCT <u>A</u> CGGGGCGG	6384
Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG	ACGTCTTTTCTCTCTCTCCTACGCAGTGGATTAATCGGCATGGCGG CTCTGGCCACGTCG <u>T</u> AGCTCGTCGCAACGCGCGCCGGCCTGGGC GTCCCGGACGCGTCCACGTTCCGCCGCGGCG	6385
	CGCCGCGGGCGGAACGTGGACGCGTCCGGGACGCCAGGCCGGC GCGCGTTGCGACGAGCT <u>A</u> CGACGTGGCCAGAGCCGCCATGCCGA TTAATCCAAGTGCCTAGGAGAGAGAGAAAAGACGT	6386
	CCACGTCG <u>T</u> AGCTCGTC	6387
	GACGAGCT <u>A</u> CGACGTGG	6388
Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG	GTCGCAACGCGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGT TCCGCCGCGGGCGCCGCGT <u>A</u> GGGCCTGAGGGGGGCGCCGGGCGTC GGCGGCGGGGACACGCTCAGCATGCGGACCAGCG	6389
	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCGCCGACGCCCG GGCCCCCTCAGGCCCT <u>A</u> CGCGGCGCGCGCGGGAACGTGGAC GCGTCCGGGACGCCAGGCCGGCGCGCGTTGCGAC	6390
	GCGCCGCGT <u>A</u> GGGCCTG	6391
	CAGGCCCT <u>A</u> CGCGGCGC	6392
Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG	TCCCGGACGCGTCCACGTTCCGCCGCGGGCGCCGCGCAGGGCCT GAGGGGGGCGCCGGGCGT <u>A</u> GGCGGCGGCGACACGCTCAGCATG CGGACCAGCGCGCGCGCGGGCGCCAGGCACCAGCA	6393
	TGCTGGTGCCTGGGCGCCGCGCGCGCTGGTCCGCATGCTGA GCGTGTCCGCCCGCCCT <u>A</u> CGCCCGGGCCCCCTCAGGCCCTG CGCGGCGCGCGGGCGGAACGTGGACGCGTCCGGGA	6394
	CCGGGCGT <u>A</u> GGCGGCGG	6395
	CCGCCGCC <u>T</u> ACGCCCGG	6396
Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG	GCGTCGGCGGGCGGGCGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGGGCGCCAGGCAC <u>T</u> AGCAGCAGGCGCGCCGCGGGGCA GGTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	6397
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCC GCGGCGCGCCTGCTGCT <u>A</u> GTGCCTGGGCGCGCGCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCGCCGACGC	6398
	CCAGGCAC <u>T</u> AGCAGCAG	6399
	CTGCTGCT <u>A</u> GTGCCTGG	6400

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS <i>Zea mays</i> Gln58Term CAG-TAG	TCGGCGGCGGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	6401
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	6402
	GGCACCAGTAGCAGGCG	6403
	CGCCTGCTACTGGTGCC	6404

Example 11**Altering fatty acid content of plants**

Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearyl- and oleoyl-ACP.

A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearyl-acyl carrier protein (stearyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 22
Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTTCCTGTACCATCTTCTTCACTT GATCCTAATGGAAAAGGCAATAAGATTGG CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACTACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAA	6405 6406

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTACGT <u>A</u> GTCAATTCT	6407
	AGAATGACT <u>T</u> ACGTAGCA	6408
5 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGTCGT <u>G</u> ATTCTTTCTGTACCATCTTCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	6409
	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAGAAT <u>C</u> ACGACGTAGCAGAGGTGGCCACCATGACGA GGAGATGAAGCGTTCAAAGACACTGCCACC	6410
	TACGTCGT <u>G</u> ATTCTTTC	6411
	GAAAGAAT <u>C</u> ACGACGTA	6412
	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCC TGTACCATCTTCTT <u>G</u> ACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATTC	6413
10 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA	GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC CATTAGGATCAAGT <u>C</u> AAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT	6414
	ATCTTCTT <u>G</u> ACTTGATC	6415
	GATCAAGT <u>C</u> AAGAAGAT	6416
	GTGGCCACCTCTGCTACGTCGTCATTCTTTCTGTACCATCTTCTT CACTTGATCCTAAT <u>T</u> GAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTAACTCTG	6417
15 Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAA TCTTATTGCCTTTTC <u>A</u> ATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAATGACGACGTAGCAGAGGTGGCCAC	6418
	ATCCTAAT <u>T</u> GAAAAGGC	6419
	GCCTTTTC <u>A</u> ATTAGGAT	6420
	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGC TACTGCCGCCACGT <u>G</u> ATCATTCTTTCCGTTGACTTCCCCTTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG	6421
20 Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA	CCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAAGTC AACGGAAAGAATGAT <u>C</u> ACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAACCAATCAGATCACAAATTCAAGC	6422
	CGCCACGT <u>G</u> ATCATTCT	6423
	AGAATGAT <u>C</u> ACGTGGCG	6424

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGTCATGATTCTTTCCGTTGACTTCCCCTTCTGGGGAT GCCAATCGGGCAATCCCGGAAAAGGGTC	6425
	GACCCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAATCATGACGTGGCGGCAGTAGCAACCATTGTG GCCACAATTAACCAATCAGATCACAATTCA	6426
	CACGTCATGATTCTTTC	6427
	GAAAGAATCATGACGTG	6428
10 Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTTCCGTAGACTTCCCCTTCTGGGGATGCCAATCGG GCAATCCCGGAAAAGGGTCGGTGAGTTTTGG	6429
	CCAAACTCACCGACCCTTTTCCGGGATTGCCCGATTGGCATCC CCAGAAGGGGAAGTCTACGGAAAGAATGATGACGTGGCGGCAGT AGCAACCATTGTGGCCACAATTAACCAATCAG	6430
	CTTCCGTAGACTTCCC	6431
	GGGAAGTCTACGGAAAG	6432
15 Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Lys21Term AAA-TAA	ATGGTTGCTACTGCCGCCACGTCATCATTCTTCCGTTGACTTCCC CTTCTGGGGATGCCAATCGGGCAATCCCGGAAAAGGGTCGGTG AGTTTTGGGTCAATGAAGTCGAAATCCGCGG	6433
	CCGCGGATTCGACTTCATTGACCCAAAACCTACCGACCCTTTTCC GGGATTGCCCGATTAGGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGCAGTAGCAACCAT	6434
	GGGATGCCCTAATCGGGC	6435
	GCCCGATTAGGCATCCC	6436
20 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG	GGGATTCAGCACGAAATTGAAGTTGTTTTAAAAACCATGGTTGC TACTGCTGTGACATAGGCGTTTTTCCAGTCACTTCTTCACCTGAC TCCTCTGACTCGAAAAACAAGAAGCTCGG	6437
	CCGAGCTTCTTGTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCCATATGTACACAGCAGTAGCAACCATGGTTTTTA AAAACAACCTCAATTCGTGCTGAAATCCC	6438
	TGTGACATAGGCGTTTT	6439
	AAAACGCCATATGTCACA	6440
25 Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT CCCAGTCACTTCTTGACCTGACTCCTCTGACTCGAAAAACAAGAAG CTCGGAAGCATCAAGTCGAAGCCATCGGT	6441
	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTCGAGT CAGAGGAGTCAGGTCAAGAAGTGACTGGGAAAAACGCCGATGTCA CAGCAGTAGCAACCATGGTTTTTAAAAACA	6442

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	CACTTCTTGACCTGACT	6443
	AGTCAGGTCAAGAAGTG	6444
	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG	6445
	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACC TGACTCCTCTGACTAGAAAAACAAGAAGCTCGGAAGCATCAAGTC GAAGCCATCGGTTTCTTCTGGAAGTTTGCA	6446
	TGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCGGA GCTTCTTGTTTTCTAGTCAGAGGAGTCAGGTGAAGAAGTGACTGG GAAAAACGCCGATGTCACAGCAGTAGCAA	6447
10	CTCTGACTAGAAAAACA	6448
	TGTTTTCTAGTCAGAG	6449
	Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA	6450
	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTG ACTCCTCTGACTCGTAAAACAAGAAGCTCGGAAGCATCAAGTCGA AGCCATCGGTTTCTTCTGGAAGTTTGCAAG	6451
	CTTGCAAACCTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGTTTTACGAGTCAGAGGAGTCAGGTGAAGAAGTGAC TGGGAAAAACGCCGATGTCACAGCAGTAGC	6452
15	CTGACTCGTAAAACAAG	6453
	CTTGTTTTACGAGTCAG	6454
	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG	6455
	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG CATTCTTCCCGTGTAGTCCCGGTACCTCCTCTAGACCAGGAA AGCCCGGAAATGGGTCATCGAGCTTCAGCCC	6456
	GGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCTAGAG GAGGTGACCGGGGACTACACGGGGAAGAATGCAGAGCTTGCAGC GGTAGCCACCATTGTCTTTCAACGAGCGGGAG	6457
20	CCCCGTGTAGTCCCGG	6458
	CCGGGGACTACACGGGG	6459
	Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA	6460
	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCGTGTCTCC CCGGTCACCTCCTCTGACCAGGAAAGCCCGGAAATGGGTCATCG AGCTTCAGCCCCATCAAGCCCAAATTTGTCG	6461
	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTT CGGGCTTTCCTGGTCAAGAGGAGGTGACCGGGGACGACACGGG GAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	6462
	CCTCCTCTGACCAGGA	6463
	TCCTGGTCAAGAGGAGG	6464

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCATGAAAGCCCCGAAATGGGTATCGAGCTTC AGCCCCATCAAGCCCCAAATTTGTCGCCAATG	6461
	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACC CATTTCCGGGCTTTCAATGGTCTAGAGGAGGTGACCGGGGACGAC ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	6462
	CTAGACCATGAAAGCCC	6463
	GGGCTTTCAATGGTCTAG	6464
10 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCAGGATAGCCCCGAAATGGGTATCGAGCTTCAGC CCCATCAAGCCCCAAATTTGTCGCCAATGGCG	6465
	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATG ACCCATTTCCGGGCTATCCTGGTCTAGAGGAGGTGACCGGGGAC GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	6466
	GACCAGGATAGCCCCGA	6467
	TCCGGGCTATCCTGGTC	6468
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCGTGAAAGCTCGGAAATGGGTATCGAGCTTG AGCCCCCTCAAGCCCCAAATTTGTCGCCAATG	6469
	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACC CATTTCCGAGCTTTACCGGCCTAGAGGAGGTGTCCGGGGACGGC AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	6470
	CTAGGCCGTGAAAGCTC	6471
	GAGCTTTCACCGCCTAG	6472
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGGATAGCTCGGAAATGGGTATCGAGCTTGAGC CCCCTCAAGCCCCAAATTTGTCGCCAATGCCG	6473
	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGAT GACCCATTTCCGAGCTATCCCGGCCTAGAGGAGGTGTCCGGGGA CGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	6474
	GGCCGGGATAGCTCGGA	6475
	TCCGAGCTATCCCGGCC	6476
25 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly26Term GGA-TGA	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCT AGGCCGGGAAAGCTCTGAAATGGGTATCGAGCTTGAGCCCCCT CAAGCCCCAAATTTGTCGCCAATGCCGGGTGA	6477
	TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGC TCGATGACCCATTTACAGAGCTTTCCCGGCCTAGAGGAGGTGTCCG GGGACGGCAGGGGGAAGAATGCAGAACTTGC	6478

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCTCTGAAATGGG	6479
	CCCATTTCAAGAGCTTTC	6480
Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTGAAGGTTAAGGC	6481
	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGATCACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	6482
	AAATGGGTGATCGAGCT	6483
	AGCTCGATCACCCATTT	6484
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGTAGCTGTTTCCGGTTTCTTCCCCAAACCTCA CTCTGGAGCCAAGACATCTGATAAGCTTGG	6485
	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG	6486
	TACTGCGTAGCTGTTTC	6487
	GAAACAGCTACGCAGTA	6488
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA	AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCATAACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	6489
	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTTATGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAACACT	6490
	CTTCCCCATAACCTCAC	6491
	GTGAGGTTATGGGGAAG	6492
Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCTTGAGCCAAGACATCTGATAAGCTTGGAGGTGA ACCAGGTAGTGTTGCTGTGCGCGGAATCA	6493
	TGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTTGGCTCAAGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	6494
	CTCACTCTTGAGCCAAG	6495
	CTTGGCTCAAGAGTGAG	6496

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC CTCACTCTGGAGCCTAGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTTGCTGTGCGCGGAATCAAGACAA	6497
	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAG CTTATCAGATGTCTAGGCTCCAGAGTGAGGTTTTGGGGAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	6498
	CTGGAGCCTAGACATCT	6499
	AGATGTCTAGGCTCCAG	6500
10 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCCTTAACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCTTGAAGCCCAAGTCAA	6501
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATGACCAGTTGC CTAACTTCCCAGGTTAAGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	6502
	CCTCCCCCTTAACCTGGG	6503
	CCCAGGTTAAGGGGAGG	6504
15 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys24Term AAG-TAG	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCAGGAGCC TCCCCTAAACCTGGGTAGTTAGGCAACTGGTCATCGAGTTTGAGC CCTTCCTTGAAGCCCAAGTCAATCCCCAATG	6505
	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATG ACCAGTTGCCTAACTACCCAGGTTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACTTGCTGCAGC	6506
	AACCTGGGTAGTTAGGC	6507
	GCCTAACTACCCAGGTT	6508
20 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCAGGAGCCTCCCCTAAACCTGG GAAGTTAGGCAACTGATCATCGAGTTTGAGCCCTTCTTGAAGCC CAAGTCAATCCCCAATGGCGGATTTAGGTT	6509
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACCTCGATGATCAGTTGCCTAACTTCCCAGGTTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA	6510
	GGCAACTGATCATCGAG	6511
	CTCGATGATCAGTTGCC	6512
25 Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Ser29Term TCA-TGA	CATGCTTCCCTGTTCCATCCCAGGAGCCTCCCCTAAACCTGGGA AGTTAGGCAACTGGTGATCGAGTTTGAGCCCTTCTTGAAGCCCA AGTCAATCCCCAATGGCGGATTTAGGTTAA	6513
	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAAACCTCGATCACCAGTTGCCTAACTTCCCAGGTTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG	6514

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5	CAACTGGT <u>G</u> ATCGAGTT	6515
	AACTCGAT <u>C</u> ACCAGTTG	6516
	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACC CCGGGAATCTCCCCTTAACCCGGGAAGTTCCGTAATGGTGGCTTT CAGGTTAAGGCAAACGCCAATGCCCATCCTA	6517
	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTAC CGAACTTCCCGGGTTAAGGGGAGATTCCCGGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCGGCAGCCACCAT	6518
	TCTCCCCTTAACCCGGG	6519
10	CCCGGGTTAAGGGGAGA	6520
	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATC TCCCCTAAACCCGGGTAGTTCGGTAATGGTGGCTTTCAGGTTAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	6521
	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCC ACCATTACCGAACTACCCGGGTTTAGGGGAGATTCCCGGGGTTGG AACGGAGAAGAATGCAGAACTTGCTGCGGC	6522
	AACCCGGGTAGTTCGGT	6523
	ACCGAACTACCCGGGTT	6524
15	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTC GGTAATGGTGGCTTTTAGGTTAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	6525
	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGG CGTTTGCCTTAACCTAAAAGCCACCATTACCGAACTTCCCGGGTTT AGGGGAGATTCCCGGGGTTGGAACGGAGAA	6526
	GTGGCTTTTAGGTTAAG	6527
	CTTAACCTAAAAGCCAC	6528
20	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAAT GGTGGCTTTCAGGTTTAGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA	6529
	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGG CATTGGCGTTTGCCTAACCTGAAAGCCACCATTACCGAACTTCCC GGGTTTAGGGGAGATTCCCGGGGTTGGAAC	6530
	TTCAGGTTTAGGCCAAC	6531
	GTTTGCCTAACCTGAA	6532

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAAATGCGACTGATAAGTTACAGACCCTCT TCTCGCATTCTCATTAACCCGGATCCGGCACACCCGGAGAACCCTCT CCTCCGTGTCGTGCTCTCATCTGAGGAAAC	6533
	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGT GTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAAC TATCAGTCGCATTACACGAGAGCTTCAACAT	6534
	ATTCTCATTAACCCGGAT	6535
	ATCCGGTTAATGAGAAT	6536
10 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGG ATCCGGCACACCCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATC TGAGGAAACCGGTTCTCGATCCTTTGCGAG	6537
	CTCGCAAAGGATCGAGAACCGGTTTCTCAGATGAGAGCACGACA CGGAGGAGACGGTTCACCGGTGTGCCGGATCCGGTTGATGAGAA TGCGAGAAGAGGGTCTGTAACCTATCAGTCGC	6538
	CACACCGGTGAACCGTC	6539
	GACGGTTCACCGGTGTG	6540
15 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCCGGATCCGGCACACCCGGAGAA CCGTCTCCTCCGTGTAGTGCTCTCATCTGAGGAAACCGGTTCTCG ATCCTTTGCGAGCGATCGTATCTGCTGATCA	6541
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGC CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	6542
	CTCCGTGTAGTGCTCTC	6543
	GAGAGCACTACACGGAG	6544
20 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA	CTTCTCGCATTCTCATCAACCCGGATCCGGCACACCCGGAGAACCGT CTCCTCCGTGTCGTGATCTCATCTGAGGAAACCGGTTCTCGATCC TTTGCGAGCGATCGTATCTGCTGATCAAGGA	6545
	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG TGCCGGATCCGGTTGATGAGAATGCGAGAAG	6546
	GTGTCGTGATCTCATCT	6547
	AGATGAGATCACGACAC	6548
25 Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGG GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACCTTAC ACACCTTCTCCTTCTTCTCCGATTCTC	6549
	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTATGGTTC CTGAGGTTTTGGTTTATAGAAGAAGAAT	6550

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGT <u>A</u> GAAGCTTT	6551
	AAAGCTTC <u>T</u> ACATTTTT	6552
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGG CATCAAAAATGTTGTAGCTTTTCGTGTAATGTGACTAACAACCTTACAC ACCTTCTCCTTCTTCTCCGATTCTCCC	6553
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA CATTACACGAAAGCT <u>A</u> CAACATTTTTGATGCCCTTTTTTTTTATGG TTCCTGAGGTTTTGGTTTATAGAAGAAGA	6554
	AAATGTTGTAGCTTTTCG	6555
	CGAAAGCT <u>A</u> CAACATTT	6556
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAA AATGTTGAAGCTTT <u>A</u> GTGTAATGTGACTAACAACCTTACACACCTTCT CCTTCTTCTCCGATTCTCCCTTTTCAT	6557
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTG TTAGTCACATTACAC <u>T</u> AAAGCTTCAACATTTTTGATGCCCTTTTTTTT TTATGGTTCCTGAGGTTTTGGTTTATAG	6558
	GAAGCTTT <u>A</u> GTGTAATG	6559
	CATTACAC <u>T</u> AAAGCTTC	6560
Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAAAATG TTGAAGCTTTTCGTG <u>A</u> AATGTGACTAACAACCTTACACACCTTCTCCTT CTTCTCCGATTCTCCCTTTTCATCCCG	6561
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA AGTTGTTAGTCACATT <u>T</u> CACGAAAGCTTCAACATTTTTGATGCCCTT TTTTTTTTATGGTTCCTGAGGTTTTGGTTT	6562
	CTTTCGTG <u>A</u> AATGTGAC	6563
	GTCACATT <u>T</u> CACGAAAG	6564

Table 23
Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 10 Increased stearate stearyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATC CAGAAATGGCTCTATAGTTTAACCCCTTTGGTGGCATCTCAGCCTTA CAAATTCCCTTCCTCGACTCGTCCGCCAA	6565
	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCCA CCAAAGGGTTAAACTATAGAGCCATTTCTGGATATGATGAATGAAT CCTTCTTTTCTACAGAGCTAGAGCTCTCCC	6566
	TGGCTCTATAGTTTAAC	6567
	GTAAACTATAGAGCCA	6568
15 Increased stearate stearyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCT AAAGTTTAACCCCTTAGGTGGCATCTCAGCCTTACAAATTCCTTCC TCGACTCGTCCGCCAACTCCTTCTTTCAG	6569
	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTAA GGCTGAGATGCCACCTAAGGGTTAACTTTAGAGCCATTTCTGGAT ATGATGAATGAATCCTTCTTTTCTACAGAG	6570
	TAACCCCTTAGGTGGCAT	6571
	ATGCCACCTAAGGGTTA	6572
20 Increased stearate stearyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACC CTTTGGTGGCATCTTAGCCTTACAAATTCCTTCCCTCGACTCGTCC GCCAACTCCTTCTTTCAGATCTCCCAAGT	6573
	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTTGTAAGGCTAAGATGCCACCAAAGGGTTAACTTTAGAG CCATTTCTGGATATGATGAATGAATCCTTCT	6574
	TGGCATCTTAGCCTTAC	6575
	GTAAGGCTAAGATGCCA	6576
25 Increased stearate stearyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCCTTTGGTG GCATCTCAGCCTTAGAAATTCCTTCCCTCGACTCGTCCGCCAACTC CTTCTTTCAGATCTCCCAAGTTCCTCTGC	6577
	GCAGAGGAAGTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGAATTTCTAAGGCTGAGATGCCACCAAAGGGTTAA ACTTTAGAGCCATTTCTGGATATGATGAATGA	6578
	CAGCCTTAGAAATCCC	6579
	GGGAATTTCTAAGGCTG	6580

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AAAGAAAATGGCATAGAAGCTTAACCCTTTGGCATCTCAGCCTTAC AAACTCCCTTCCTCGGCTCGTCCGCCAAT	6581
	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGATGC CAAAGGGTTAAGCTTCTATGCCATTTTCTTTTTTTGATACGAGGTT TGATGTTCTTTCAGACACGAGCGAGCTCTC	6582
	AATGGCATAGAAGCTTA	6583
	TAAGCTTCTATGCCATT	6584
10 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AGAAAATGGCATTGTAGCTTAACCCTTTGGCATCTCAGCCTTACAA ACTCCCTTCCTCGGCTCGTCCGCCAATCT	6585
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGAT GCCAAAGGGTTAAGCTACAATGCCATTTTCTTTTTTTGATACGAG GTTTGATGTTCTTTCAGACACGAGCGAGCTC	6586
	TGGCATTGTAGCTTAAC	6587
	GTTAAGCTACAATGCCA	6588
15 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAGAAAATGGCATT GAAGCTTAACCCTTAGGCATCTCAGCCTTACAACTCCCTTCCTCG GCTCGTCCGCCAATCTCTACTCTCAGATC	6589
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT GTAAGGCTGAGATGCCAAGGGTTAAGCTTCAATGCCATTTTCTTT TTTTTGATACGAGGTTTGATGTTCTTTCAGA	6590
	TAACCCTTAGGCATCTC	6591
	GAGATGCCAAGGGTTA	6592
20 Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAGAAAATGGCATTGAAGCTTAA CCCTTTGGCATCTTAGCCTTACAACTCCCTTCCTCGGCTCGTCCG CCAATCTCTACTCTCAGATCTCCCAAGT	6593
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTTGTAAAGGCTAAGATGCCAAGGGTTAAGCTTCAATGCC ATTTCTTTTTTTGATACGAGGTTTGATGTT	6594
	TGGCATCTTAGCCTTAC	6595
	GTAAGGCTAAGATGCCA	6596
25 Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA	AACCAAAAGAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCA ATCCTTTCTTTCTTAAACCAAAAGTTACCTTCTTTCGCTCTTCCA CCAATGGCCAGTACCAGATCTCCTAAGT	6597
	ACTTAGGAGATCTGGTACTGGCCATTGGTGAAGAGCGAAAGAAG GTAACCTTTGGGTTTAAAGAAAGGAAAGGATTGAGCTTGAGAGCCAT TGTTTTTTTCTTACCTTTTTCTTTTGTT	6598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	TCCTTTCTTAAACCCAA	6599
	TTGGGTTTAAAGAAAGGA	6600
5 Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA	AAGAAAAAGGTAAGAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTTCTCAAACCTAAAAGTTACCTTCTTTGCTCTTCCACCAATG GCCAGTACCAGATCTCCTAAGTTCTACA	6601
	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGA AAGAAGGTAACTTTTAGGTTTGAGAAAGGAAAGGATTGAGCTTGAG AGCCATTGTTTTTTTCTTACCTTTTTCTT	6602
	CTCAAACCTAAAAGTTA	6603
	TAACTTTTAGGTTTGAG	6604
10 Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG	AAAAAGGTAAGAAAAAACAATGGCTCTCAAGCTCAATCCTTTCC TTTCTCAAACCCAATAGTTACCTTCTTTGCTCTTCCACCAATGGC CAGTACCAGATCTCCTAAGTTCTACATGG	6605
	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAG CGAAAGAAGGTAACATAAGGTTTGAGAAAGGAAAGGATTGAGCT TGAGAGCCATTGTTTTTTTCTTACCTTTTT	6606
	AAACCCAATAGTTACCT	6607
	AGGTAACATAAGGTTT	6608
15 Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG	TCTCAAACCCAAAGTTACCTTCTTTGCTCTTCCACCAATGGCCA GTACCAGATCTCCTAGTTCTACATGGCCTCTACCCTCAAGTCTGG TTCTAAGGAAGTTGAGAATCTCAAGAAGC	6609
	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGA GGCCATGTAGAACTAAGGAGATCTGGTACTGGCCATTGGTGGAAG AGCGAAAGAAGGTAACTTTTGGGTTTGAGA	6610
	GATCTCCTTAGTTCTAC	6611
	GTAGAACTAAGGAGATC	6612
20 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA	TCTTCTGATTCAITTAATCTTTACTCATCAATGGCTCTGAGACTGAA CCCTATCCCCACCTAAACCTTCTCCCTCCCCCAAATGGCCAGTCT CAGATCTCCCAGGTTCCGCATGGCCTCTA	6613
	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGG GGGAGGGAGAAGGTTTAGGTGGGGATAGGGTTCAGTCTCAGAGC CATTGATGAGTAAAGATTAAATGAATCAGAAGA	6614
	TCCCCACCTAAACCTTC	6615
	GAAGGTTTAGGTGGGGA	6616

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAA CCTTCTCCCTCCCCTAAATGGCCAGTCTCAGATCTCCCAGGTTCC GCATGGCCTCTACCCTCCGCTCCGGTTCCA	6617
	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTTAGGGGAGGGAGAAGGTTTGGGTGGGGAT AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	6618
	CCCTCCCCTAAATGGCC	6619
	GGCCATTTAGGGGAGGG	6620
10 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	6621
	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTTGGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	6622
	CCAGTCTCTGATCTCCC	6623
	GGGAGATCAGAGACTGG	6624
15 Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCTAAGAGGTTGAAAATATTAAGAAGCCATTCA CTCCTCCCAGAGAAGTGCATGTTCAAGTAA	6625
	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAAT ATTTTCAACCTCTTAGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATCTGAGACTGGCCATTTG	6626
	CCGGTTCCTAAGAGGTT	6627
	AACCTCTTAGGAACCGG	6628
20 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATCA ATACGGCGACGTTTAAATCAGACCTGTACCGTTCATTGCGGTTTCC TCAACCGAAACCTCTCAGATCTCCCAAAT	6629
	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAAC GGTACAGGTCTGATTAAACGTCGCCGTATTGATGCGAATCGCCA TTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	6630
	CGACGTTTAAATCAGAC	6631
	GTCTGATTAAACGTCG	6632
25 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser12Term TCA-TGA	AAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATCAATAC GGCGACGTTTCAATGAGACCTGTACCGTTCATTGCGGTTTCCCAA CCGAAACCTCTCAGATCTCCCAAATTCGC	6633
	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAAT GAACGGTACAGGTCTCATTGAAACGTCGCCGTATTGATGCGAATC GCCATTGTTGATGTTGTTCTTGTGTGTGCTT	6634

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAAT <u>G</u> AGACCTGT	6635
	ACAGGTCT <u>C</u> ATTGAAAC	6636
5 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG	AAGAACAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTT CAATCAGACCTGTAG <u>C</u> GTTTCATTTCGCGTTTCCTCAACCGAAACCTC TCAGATCTCCCAAATTCGCCATGGCTTCC	6637
	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG AAACGCGAATGAACG <u>C</u> TACAGGTCTGATTGAAACGTCGCCGTATT GATGCGAATCGCCATTGTTGATGTTGTTCTT	6638
	GACCTGTAG <u>C</u> GTTTCATT	6639
	AATGAACG <u>C</u> TACAGGTC	6640
10 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA	CAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTTCAATC AGACCTGTACCGTT <u>G</u> ATTTCGCGTTTCCTCAACCGAAACCTCTCAGA TCTCCCAAATTCGCCATGGCTTCCACCAT	6641
	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT TGAGGAAACGCGAAT <u>C</u> AACGGTACAGGTCTGATTGAAACGTCGCC GTATTGATGCGAATCGCCATTGTTGATGTTG	6642
	GTACCGTT <u>G</u> ATTTCGCGT	6643
	ACGCGAAT <u>C</u> AACGGTAC	6644
15 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC AACGATGGCGCTT <u>T</u> GAAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATACACTTTTCATCAATCGA	6645
	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT CACCGGACTCATT <u>C</u> AAGCGCCATCGTTGATGAAGAAGATGATGA TGTGTGTGTGATTGAGTGTGTGTTGTGTGT	6646
	TGGCGCTT <u>T</u> GAAATGAGT	6647
	ACTCATTC <u>A</u> AAGCGCCA	6648
20 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA GTCCGGTGACGCTT <u>T</u> AACGGGAGATATATCCTTCATACACTTTTCA TCAATCGAAAAATCTCAGATCTCCTAAAT	6649
	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG ATATATCTCCCGTT <u>A</u> AAGCGTCACCGGACTCATTGGAAGCGCCAT CGTTGATGAAGAAGATGATGATGTGTGTGT	6650
	TGACGCTT <u>T</u> AACGGGAG	6651
	CTCCCGTT <u>A</u> AAGCGTCA	6652

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG TGACGCTTCAACGGTAGATATATCCTTCATACACTTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTCGCGA	6653
	TCGCGAATTTAGGAGATCTGAGATTTTCGATTGATGAAAAGTGTA TGAAGGATATATCTACCGTTGAAGCGTCACCGGACTCATTCTGAAG CGCCATCGTTGATGAAGAAGATGATGATGT	6654
	TTCAACGGTAGATATAT	6655
	ATATATCTACCGTTGAA	6656
10 Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTT CAACGGGAGATATAGCCTTCATACACTTTTCATCAATCGAAAAATCT CAGATCTCCTAAATTCGCGATGGCTTCC	6657
	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTCGATTGATGA AAAGTGTATGAAGGCTATATCTCCCGTTGAAGCGTCACCGGACTC ATTCGAAGCGCCATCGTTGATGAAGAAGAT	6658
	GAGATATAGCCTTCATA	6659
	TATGAAGGCTATATCTC	6660
15 Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG	AACTCAGCCAGCTTGCCCCAAACAACAGCGCAGAAAAACCTTCA ACAACAATGGCTCTCTAGCTCAACCCAGTCACCACCTTCCCTTCAA CACGCTCCCTCAACAACCTTCTCCTCCAGAT	6661
	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTGGAAGGGAAGGTG GTGACTGGGTTGAGCTAGAGAGCCATTGTTGTTGAAGGTTTTCTG CGCTGTTGTTGGGGCAAGCTGGCTGAGTT	6662
	TGGCTCTCTAGCTCAAC	6663
	GTTGAGCTAGAGAGCCA	6664
20 Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTTCCCTTGAACACGCTCCCTCAACAACCTTCTCCTCCAG ATCTCCTCGCACCTTTCTCATGGCTGCTTC	6665
	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGTTCAGGGGAAGGTGGTGAAGTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTTCTGCGC	6666
	CTTCCCTTGAACACGCT	6667
	AGCGTGTTCAAGGGAAG	6668
25 Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTC ACAACCTTCTCCTCCTGATCTCCTCGCACCTTTCTCATGGCTGCTT CCACTTTCAATTCCACCTCCACCAAGTAAG	6669
	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAA AGGTGCGAGGAGATCAGGAGGAGAAGTTGTTGAGGGAGCGTGT GAAGGGAAGGTGGTGAAGTGGGTTGAGCTTGAG	6670

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5	TCTCCTCC <u>T</u> GATCTCCT	6671
	AGGAGATC <u>A</u> GGAGGAGA	6672
	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCACCT <u>A</u> GTAAAGCATCTCCTCCTCCTCGGAATCTCCG CCGATTTCTTTTAAGCGATTGATCGTAGA	6673
	TCTACGATCAATCGCTTAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACT <u>A</u> GGTGGAGGTGGAATTGAAAGTGGAAGCAG CCATGAGAAAGGTGCGAGGAGATCTGGAGGA	6674
	CCTCCACCT <u>A</u> GTAAAGCA	6675
	TGCTTACT <u>A</u> GGTGGAGG	6676
10	ATGGCACTGAACTTTGCTTTCCACCCCACAAGATGCCTTCCTTCC CCGATGCTCGTATCT <u>T</u> GATCTCACAGGGTTTTTCATGGCTTCAACTAT TCATTCTCCTTCTATGGAGGTCGGAAG	6677
	CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCTGTGAGATC <u>A</u> GATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTTCAGTGCCAT	6678
	CTCGTATC <u>T</u> GATCTCAC	6679
	GTGAGATC <u>A</u> GATACGAG	6680
15	CCCACAAGATGCCTTCCTTCCCCGATGCTCGTATCAGATCTCACA GGGTTTTTCATGGCTT <u>G</u> AACTATTCACTTCTCCTTCTATGGAGGTCGG AAAAGTTAAAAAGCCTTTACGCCTCCACG	6681
	CGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCTCCATAGAAG GAGAATGAATAGTT <u>C</u> AAGCCATGAAAACCCTGTGAGATCTGATACG AGCATCGGGGAAGGAAGGCATCTTGTGGG	6682
	CATGGCTT <u>G</u> AACTATTC	6683
	GAATAGTT <u>C</u> AAGCCATG	6684
20	GATGCTCGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTC ATTCTCCTTCTATGT <u>A</u> GGTCGGAAGTTAAAAAGCCTTTACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	6685
	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTTT AACTTTTCCGACCT <u>A</u> CATAGAAGGAGAATGAATAGTTGAAGCCATG AAAACCCTGTGAGATCTGATACGAGCATC	6686
	CTTCTATGT <u>A</u> GGTCGGA	6687
	TCCGACCT <u>A</u> CATAGAAG	6688

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTCATTCTC CTTCTATGGAGGTCTGAAAAGTTAAAAAGCCTTTCACGCCTCCACG AGAGGTACATGTTCAAGTAACCCATTCTT	6689
	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAG GCTTTTTAACTTTTCAGACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCCTGTGAGATCTGATACG	6690
	TGGAGGTCTGAAAAGTT	6691
	AACTTTTCAGACCTCCA	6692
10 Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA	TTCTCGTTTTTGTCTGCCCTCTGCTCTCTCTCTATCAGGCACG GAGAAATGGCACTGTAACTCAGTCCAGTCATGTTTCAATCTCAGAA GCTTCCATTTCTTGCTCCTATCCGCCTT	6693
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACA TGA CTGGACTGAGTTACAGTGCCATTTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGGACGACAAAACGAGAA	6694
	TGGCACTGTAACTCAGT	6695
	ACTGAGTTACAGTGCCA	6696
15 Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA	CTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTC AGTCCAGTCATGTTTAACTCTCAGAAGCTTCCATTTCTTGCTCCTA TCCGCCTTCCAATCTCAGATCTCCGAGGG	6697
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTTCTGAGATTAAAACATGACTGGACTGAGTTTCAGTGCCA TTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	6698
	TCATGTTTAACTCTCAG	6699
	CTGAGATTAAAACATGA	6700
20 Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTTTCAATCTTAGAAGCTTCCATTTCTTGCTCCTATCCGC CTTCCAATCTCAGATCTCCGAGGGTTTTCA	6701
	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCTTCTAAGATTGAAACATGACTGGACTGAGTTTCAG TGCCATTTCTCCGTGCCTGATAGAGAGAGA	6702
	TTCAATCTTAGAAGCTT	6703
	AAGCTTCTAAGATTGAA	6704
25 Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTTTCAATCTCAGTAGCTTCCATTTCTTGCTCCTATCCGCCTTC CAATCTCAGATCTCCGAGGGTTTTTCATGG	6705
	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGG CAAGAAATGGAAGCTACTGAGATTGAAACATGACTGGACTGAGTTT CAGTGCCATTTCTCCGTGCCTGATAGAGAG	6706

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCTCAGTAGCTTCCA	6707
	TGGAAGCTACTGAGATT	6708
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC ACACCGCATCGCCGTAGTCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCAAGATGGTGGCCATGGCC	6709
	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC CACGCCGCCGAGGACTACGGCGATGCGGTGTGGGACGCCGCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	6710
	TCGCCGTAGTCCTGCGG	6711
	CCGCAGGACTACGGCGA	6712
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTACTC CTGCGGCGGCGTGGCGTAGAGGAGGAGCAATGGGATGTCAAGA TGGTGGCCATGGCCTCCACCATCAACAGGGTCA	6713
	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC CATTGCTCCTCCTCTACGCCACGCCGCCGAGGAGTACGGCGAT GCGGTGTGGGACGCCGGAACGCCATGAGCAG	6714
	GCGTGGCGTAGAGGAGG	6715
	CCTCCTCTACGCCACGC	6716
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG	CCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAG GAGGAGCAATGGGATGTAGAAGATGGTGGCCATGGCCTCCACCA TCAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	6717
	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC ATGGCCACCATCTTCTACATCCCATTGCTCCTCCTCTGCGCCACG CCGCCGCAGGAGTACGGCGATGCGGTGTGGG	6718
	TGGGATGTAGAAGATGG	6719
	CCATCTTCTACATCCCA	6720
Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG	CACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTGCTAGATGGTGGCCATGGCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	6721
	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG CCATGGCCACCATCTACGACATCCCATTGCTCCTCCTCTGCGCCA CGCCGCCGAGGAGTACGGCGATGCGGTGTG	6722
	GGATGTCGTAGATGGTG	6723
	CACCATCTACGACATCC	6724

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA GAGAAGCAATGGCGT <u>A</u> GAAGCTTCACCACACGGCCTTCAATCCTT CCATGGCGGTTACCTCTTCGGGACTTCCTCG	6725
	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTTCTACGCCATTGCTTCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTCAACCTAGAGAGAGAA	6726
	AATGGCGT <u>A</u> GAAGCTTC	6727
	GAAGCTTCTACGCCATT	6728
10 Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA GAAGCAATGGCGTTGTAGCTTCACCACACGGCCTTCAATCCTTCC ATGGCGGTTACCTCTTCGGGACTTCCTCGAT	6729
	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCT <u>A</u> CAACGCCATTGCTTCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	6730
	TGGCGTTGTAGCTTCAC	6731
	GTGAAGCT <u>A</u> CAACGCCA	6732
15 Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT GGCGGTTACCTCTT <u>A</u> GGGACTTCCTCGATCGTATCACCTCAGATC TCACCGCGTTTTTCATGGCTTCTTCTACAAT	6733
	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	6734
	TACCTCTT <u>A</u> GGGACTTC	6735
	GAAGTCCCTAAGAGGTA	6736
20 Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG GCGGTTACCTCTTCGTGACTTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTTTCATGGCTTCTTCTACAATTG	6737
	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTCA <u>A</u> CGAAGAGGTAACCGCCATGGAAGGATTGA AGGCCGTGTGGTGAAGCTTCAACGCCATTGC	6738
	CCTCTTCGTGACTTCCT	6739
	AGGAAGTCA <u>A</u> CGAAGAGG	6740
25 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCCGTTTTCCACACCATTTTCAAGTGTGTCG ATTGCCGTCTTTCTGACCTCGTCAAACGCCTTCTCGCAGATCTCCC AAATTCCTCATGGCTTCCACTCTCAGCAG	6741
	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA GGCGTTTGACGAGGT <u>C</u> AGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAACGGGGTTGAGATTCAGAGCCA	6742

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GTCTTTCTGACCTCGTC	6743
	GACGAGGTGAGAAAGAC	6744
5 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA	AATCTCAACCCCGTTTCCACACCATTTAGTGTGTCGATTGCCGT CTTTCTCACCTCGTTAAACGCCTTCTCGCAGATCTCCCAAATTCTT CATGGCTTCCACTCTCAGCAGCTCTTCTC	6745
	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC TGCGAGAAGGCGTTTAAACGAGGTGAGAAAGACGGCAATCGACGA CACTGAAATGGTGTGGAAACGGGGTTGAGATT	6746
	CACCTCGTTAAACGCCT	6747
	AGGCGTTTAAACGAGGTG	6748
10 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA	TCCACACCATTTAGTGTGTCGATTGCCGTCTTTCTCACCTCGTC AAACGCCTTCTCGCTGATCTCCCAAATTCTTCATGGCTTCCACTCT CAGCAGCTCTTCTCCTAAGGAAGCGGAAA	6749
	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGA AGAATTTGGGAGATCAGCGAGAAGGCGTTTGACGAGGTGAGAAAG ACGGCAATCGACGACACTGAAATGGTGTGGA	6750
	CTTCTCGCTGATCTCCC	6751
	GGGAGATCAGCGAGAAG	6752
15 Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA	TTTCAGTGTGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTT CTCGCAGATCTCCCTAATTCTTCATGGCTTCCACTCTCAGCAGCTC TTCTCCTAAGGAAGCGGAAAGCCTGAAGA	6753
	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGG AAGCCATGAAGAATTAGGGAGATCTGCGAGAAGGCGTTTGACGAG GTGAGAAAGACGGCAATCGACGACACTGAAA	6754
	GATCTCCCTAATTCTTC	6755
	GAAGAATTAGGGAGATC	6756
20 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATAT CAATGGGGTGTGCTGAAAAATCTCACAAAATGTTACCATTTCCTTGT TCTTCAGCCAGATCTGAGCGAGTTTTCAT	6757
	ATGAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAACA TTTTGTGAGATTTTCACGACACCCCATTTGATATTCAGTGCCATTGTT GATGCTCTGTTTTTCACTCGACTATTT	6758
	GGTGTGCTGAAAAATCTC	6759
	GAGATTTTCACGACACC	6760

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTCTGTTATAATCTCACAAATGTTACCATTTCTTGTCT TCAGCCAGATCTGAGCGAGTTTTCATGG	6761
	CCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTA ACATTTTGTGAGATTATAACGACACCCCATTTGATATTCAGTGCCATT GTTGATGCTCTGTTTTTACCTCGACTAT	6762
	TGTCGTTATAATCTCAC	6763
	GTGAGATTATAACGACA	6764
10 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA	GTGAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGT CGTTAAAATCTCACTAAATGTTACCATTTCTTGTCTTCAGCCAGA TCTGAGCGAGTTTTTATGGCTTCAACCA	6765
	TGGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAG GAAATGGTAACATTTAGTGAGATTTTAACGACACCCCATTTGATATTC AGTGCCATTGTTGATGCTCTGTTTTTAC	6766
	AATCTCACTAAATGTTA	6767
	TAACATTTAGTGAGATT	6768
15 Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCTGTTAAA ATCTCACAAAATGTGACCATTTCTTGTCTTCAGCCAGATCTGAG CGAGTTTTTATGGCTTCAACCATTCATCG	6769
	CGATGAATGGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGTCACATTTTGTGAGATTTTAACGACACCCCAT TGATATTCAGTGCCATTGTTGATGCTCTGT	6770
	CAAATGTGACCATTTCT	6771
	GAAATGGTCACATTTTG	6772
20 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCTAACCCCTTACAGAAGCTCTTCTCTC TCCTTCTTCATCATGATCTTCTTCTTCTTCATCGTTCTCGCTTCCTC AAATGGCTAGCCTCAGATCTCCAAGGTT	6773
	AACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGATCATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTACGCCTCAGAGCCA	6774
	TTCATCATGATCTTCTT	6775
	AAGAAGATCATGATGAA	6776
25 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA	ACCCTAACCCCTTACAGAAGCTCTTCTCTCTCCTTCTTCATCATCA TCTTCTTCTTCTTGATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC	6777
	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGA GGAAGCGAGAACGATCAAGAAGAAGAAGATGATGATGAAGAAGGA GAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	6778

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG	TTCTTCTTGATCGTTCT	6779
	AGAACGATCAAGAAGAA	6780
	CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT TCTTCTTCTTCATAGTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTTCCGCATGGCCTCCACCCT	6781
	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAAGCTATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	6782
	TTCTTCATAGTTCTCGC	6783
	GCGAGAACTATGAAGAA	6784
	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT TCTTCATCGTTCTAGCTTCCTCAAATGGCTAGCCTCAGATCTCCAA GGTTCCGCATGGCCTCCACCCTCCGCAC	6785
	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT AGCCATTTGAGGAAGCTAGAACGATGAAGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	6786
	ATCGTTCTAGCTTCCTC	6787
	GAGGAAGCTAGAACGAT	6788
10 Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG	AAAGTTAAAAGCCGTCCAAAACCCAAACCAGGAAAGGCCAAACGAA AAGAAAAAATGGCTTAGAATTTTAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTTGCTTTGCTCTTCCACCAAA	6789
	TTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTGAGGGCG ATGGCATTAAAATTCTAAGCCATTTTTCTTTTCGTTTGCCTTTCCT GGTTTGGGTTTTGGACGGCTTTTAACTTT	6790
	AATGGCTTAGAATTTTA	6791
	TAAAATTCTAAGCCATT	6792
	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTT TAATGCCATCGCCTAGAAATCTCAGAAGCTCCCTTGCTTTGCTCTT CCACCAAAGGCCACCCTTAGATCTCCCAA	6793
15 Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG	TTGGGAGATCTAAGGGTGGCCTTTGGTGGAAAGAGCAAAGCAAGG GAGCTTCTGAGATTTCTAGGCGATGGCATTAAAATTCAAAGCCATT TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	6794
	CATCGCCTAGAAATCTC	6795
	GAGATTTCTAGGCGATG	6796
20 Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG		

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Increased stearate stearyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAATGGCTTTGAATTTTA ATGCCATCGCCTCGTAATCTCAGAAGCTCCCTTGCTTTGCTCTTCC ACCAAAGGCCACCCTTAGATCTCCCAAGT	6797
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAAGAGCAAAGCAAG GGAGCTTCTGAGATTACGAGGCGATGGCATTAAAATTCAAAGCCA TTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	6798
	TCGCCTCGTAATCTCAG	6799
	CTGAGATTACGAGGCGA	6800
10 Increased stearate stearyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAATGGCTTTGAATTTTAATGCCA TCGCCTCGAAATCTTAGAAGCTCCCTTGCTTTGCTCTTCCACCAAA GGCCACCCTTAGATCTCCCAAGTTTCCA	6801
	TGGAAACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAAGAGCAA AGCAAGGGAGCTTCTAAGATTTGAGGCGATGGCATTAAAATTCAA AGCCATTTTTCTTTTCGTTTGCCTTTCCT	6802
	CGAAATCTTAGAAGCTC	6803
	GAGCTTCTAAGATTTG	6804

Table 24
Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	6805
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	6806
	GGCGAGCTTGGTTTTAT	6807
	ATAAAACCAAGCTCGCC	6808
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA	ACGACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTTGATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	6809
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTCTTCC CAAGAAGAAAAGAGGAAAAAGTCTCTGTCGT	6810
	CTCGGTTTGATCAGAAT	6811
	ATTCTGATCAAACCGAG	6812
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA	ACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTATGAGAATGTGGTTTTAGACCTCTCCCCAGATTCT TACCCTAAACACACAACCTCTTTTGCCTC	6813
	GAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	6814
	GGTTTTATGAGAATGTG	6815
	CACATTCTCATAAAACC	6816
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA	AGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCATTAATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	6817
	TAGAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAGAGGAAAAAGTCTCT	6818
	TTTTATCATTAATGTGGT	6819
	ACCACATTATGATAAAA	6820

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGAGCAAAAGAGCTCT AGCAATGGCGAACTAGGTCTTATCCGAATGTGGCATAAGACCTCT CCCCAGAATCTACACCACACCCAGATCCAC	6821
	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCA CATTCGGATAAGACCTAGTTTCGCCATTGCTAGAGCTCTTTTGCTCT CTCTCTCTCCCCAGAAGAAGAAGATGATGA	6822
	GGCGAACTAGGTCTTAT	6823
	ATAAGACCTAGTTTCGCC	6824
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA	TCTTCTTCTTCTGGGGAGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA TGGCGAACTTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCA GAATCTACACCACACCCAGATCCACTTTCCT	6825
	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTT ATGCCACATTCCGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTT TGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	6826
	CTTGGTCTGATCCGAAT	6827
	ATTCGGATCAGACCAAG	6828
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA	TTCTTCTGGGGAGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCG AACTTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAATCT ACACCACACCCAGATCCACTTTCCTCTCCA	6829
	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGA GGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGAG CTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA	6830
	TCTTATCCTAATGTGGC	6831
	GCCACATTAGGATAAGA	6832
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACTT GGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACAC CACACCCAGATCCACTTTCCTCTCCAACACC	6833
	GGTGTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGG GAGAGGTCTTATGCCTCATTTCGGATAAGACCAAGTTCGCCATTGCT AGAGCTCTTTTGCTCTCTCTCTCTCCCCAG	6834
	TCCGAATGAGGCATAAG	6835
	CTTATGCCCTCATTTCGGA	6836
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA	ATAACAGAAATGCTGAATTCCTTGCAATTTTAGCTTCTGGGTTTTCAA TGGCTGCTGGTTGAGTATTATCAGAATGTGGTTTAAGGCCTCTCCC AAGAATCTACTACGACCCAGAATTGGT	6837
	ACCAATTCTGGGTCTGTGAGTAGATTCTTGGGAGAGGCCTTAAACC ACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCT AAAAATGCAAGAATTCAGCAATTCTGTTAT	6838

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
	GCTGGTTGAGTATTATC	6839
	GATAATAC T CAACCAGC	6840
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCT GCTGGTTGGGTATGATCAGAATGTGGTTTAAGGCCTCTCCCAAGA ATCTACTCACGACCCAGAATTGGTTTTAC	6841
	GTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTT AAACCACATTCTGATCATAACCAACCAGCAGCCATTGAAAACCCAG AAGCTAAAAATGCAAGAATTCAGCAATTCT	6842
	TTGGGTATGATCAGAAT	6843
	ATTCTGATCATAACCAA	6844
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCT GGTTGGGTATTATGAGAATGTGGTTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTTACATC	6845
	GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGC CTTAAACCACATTCTCATAATACCAACCAGCAGCCATTGAAAACC CAGAAGCTAAAAATGCAAGAATTCAGCAAT	6846
	GGTATTATGAGAATGTG	6847
	CACATTCTCATAATACC	6848
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTG GTTGGGTATTATCATAATGTGGTTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTTACATCGA	6849
	TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAG GCCTTAAACCACATTATGATAATACCAACCAGCAGCCATTGAAAA CCCAGAAGCTAAAAATGCAAGAATTCAGCA	6850
	TATTATCATAATGTGGT	6851
	ACCACATTATGATAATA	6852
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA	GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAA TCTACCCTAAGCCCTGAAGCTGGGGCAGCCACTTCTGCCTCCTCTC ACATTAAGTTGAGAATTCACGTACAGATC	6853
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGT GGCTGCCCCAGTTCAGGGCTTAGGGTAGATTCTTGGGAGTGGTCT AAGACCACATTCTGATAAAACCAACTTGC	6854
	CTAAGCCCTGAAGCTGGG	6855
	CCCAGTTCAGGGCTTAG	6856

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCT GCCTCCTCTCACATT <u>T</u> AGTTGAGAATTTACGTACAGATCTGAGTG GTTCTGCAATTTCTTTGTCTAATACTAATA	6857
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACT <u>A</u> AATGTGAGAGGAGGCAGAAGTGGCTGCCCC AGTTCTGGGCTTAGGGTAGATTCTTGGGAG	6858
	CTCACATT <u>T</u> AGTTGAGA	6859
	TCTCAACT <u>A</u> AATGTGAG	6860
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAGT <u>A</u> GAGAATTTACGTACAGATCTGAGTGGTTC TGCAATTTCTTTGTCTAATACTAATAAAGA	6861
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTC <u>T</u> ACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGGCTTAGGGTAGATTCTTG	6862
	CATTAAGT <u>A</u> GAGAATTT	6863
	AAATTCTC <u>T</u> ACTTAATG	6864
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAGTTG <u>T</u> GAAATTTACGTACAGATCTGAGTGGTTCG CAATTTCTTTGTCTAATACTAATAAAGAGA	6865
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTC <u>A</u> CAACTTAATGTGAGAGGAGGCAGAAGTGGCT GCCCCAGTTCTGGGCTTAGGGTAGATTCT	6866
	TTAAGTTG <u>T</u> GAAATTTCA	6867
	TGAAATTC <u>A</u> CAACTTAA	6868
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGG GTCTATCCTAAGCCAT <u>T</u> GAACTGGCCACCCTTTGTTGAATTCCAATC CCACAAAGCTGAGATTTTCAAGAACAGATC	6869
	GATCTGTTCTTGAAATCTCAGCTTTGTGGGATTGGAATTCAACAA AGGGTGGCCAGTT <u>C</u> ATGGCTTAGGATAGACCCTCGGGAGTGGCC TCAGACCACATTCTGATAAAACCCAACCTCGC	6870
	CTAAGCCAT <u>T</u> GAACTGGC	6871
	GCCAGTTC <u>A</u> TGGCTTAG	6872
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAA GAACTGGCCACCCTT <u>A</u> GTTGAATTCCAATCCCACAAAGCTGAGATT TTCAAGAACAGATCTTGAAATGGTTCTTC	6873
	GAAGAACCATTTCGAAGATCTGTTCTTGAAAATCTCAGCTTTGTGG GATTGGAATTCAACT <u>A</u> AGGGTGGCCAGTTCTTGGCTTAGGATAGA CCCTCGGGAGTGGCCTCAGACCACATTCTG	6874

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG	CCACCCTT <u>A</u> GTTGAATT	6875
	AATTCAACT <u>A</u> AGGGTGG	6876
	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAA CTGGCCACCCTTTGT <u>A</u> GAATTCCAATCCCACAAAGCTGAGATTTTC AAGAACAGATCTTGGAATGGTTCTTCATT	6877
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGT GGGATTGGAATTCT <u>A</u> CACAAAGGGTGGCCAGTTCTTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	6878
	CCCTTTGT <u>A</u> GAATTCCA	6879
	TGGAATTCT <u>A</u> CACAAAGGG	6880
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTG AATTCCAATCCCACAT <u>A</u> GCTGAGATTTTCAAGAACAGATCTTGAA ATGGTTCTTCATTCTGTTTGTGAGTGGA	6881
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCT TGAAAATCTCAGCT <u>A</u> TGTGGGATTGGAATTCAACAAAGGGTGGCC AGTTCTTGGCTTAGGATAGACCCTCGGGAG	6882
	ATCCCACATAGCTGAGA	6883
	TCTCAGCT <u>A</u> TGTGGGAT	6884
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATG GAAGTCTATGAGTTA <u>G</u> GTCGTCAGAGAGCTAGCCATCGTGTTCCG ACTAGCTGCTGGAGCTGCTTACCTCAACAAT	6885
	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGC TAGCTCTCTGACGAC <u>C</u> TAACTCATAGACTTCCATGGATTCTTAACC CAGCAATGCTTAGGTATCGCCGCTCTGATG	6886
	ATGAGTTA <u>G</u> GTCGTCAG	6887
	CTGACGAC <u>C</u> TAACTCAT	6888
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA	GCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCT ATGAGTTACGTCGTC <u>T</u> GAGAGCTAGCCATCGTGTTCCGACTAGCT GCTGGAGCTGCTTACCTCAACAATTGGCTTG	6889
	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACA CGATGGCTAGCTCTC <u>A</u> GACGACGTAACCTCATAGACTTCCATGGAT TCTTAACCCAGCAATGCTTAGGTATCGCCGC	6890
	ACGTCGTC <u>T</u> GAGAGCTA	6891
	TAGCTCTC <u>A</u> GACGACGT	6892

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCTATGA GTTACGTCGTCAGATAGCTAGCCATCGTGTTGCGACTAGCTGCTG GAGCTGCTTACCTCAACAATTGGCTTGTTT	6893
	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGA ACACGATGGCTAGCTATCTGACGACGTAACCTCATAGACTTCCATG GATTCTTAACCCAGCAATGCTTAGGTATCGC	6894
	TCGTCAGATAGCTAGCC	6895
	GGCTAGCTATCTGACGA	6896
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTG TTCGCGACTAGCTGCTTGAGCTGCTTACCTCAACAATTGGCTTGTTT GGCCTCTCTATTGGATTGCTCAAGGAACCA	6897
	TGGTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACCTCATAGACTTCCATGG	6898
	TAGCTGCTTGAGCTGCT	6899
	AGCAGCTCAAGCAGCTA	6900
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA	GCAAGTTGGGTCTATCAGAATGTGGTCTTAGACCACTACCAAGAA TATACCCAAAGCCCTGAATAGGGTCTTCTTCCGTTTGCGCCACCAA TTTAAATCTGAGAAGAATTTACCTTCAC	6901
	GTGAAGGTGAAATTCCTCTCAGATTTAAATTGGTGGCGCAAACGGA AGAAGACCCTATTCAGGGCTTTGGGTATATTCTTGGTAGTGGTCTA AGACCACATTCTGATAGAACCCAACTTGC	6902
	CAAAGCCCTGAATAGGG	6903
	CCCTATTCAGGGCTTTG	6904
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG GTCTTCTTCCGTTTGAGCCACCAATTTAAATCTGAGAAGAATTTCA CCTTCACCTATACGAACAGATCGGAATTGT	6905
	ACAATTCCGATCTGTTCTGATAGGTGAAGGTGAAATTCCTCTCAGA TTTAAATTGGTGGCTCAAACGGAAGAAGACCCTATTCTGGGCTTTG GGTATATTCTTGGTAGTGGTCTAAGACCA	6906
	TCCGTTTGAGCCACCAA	6907
	TTGGTGGCTCAAACGGA	6908
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGT TTGCGCCACCAATTGAAATCTGAGAAGAATTTACCTTCACCTATA CGAACAGATCGGAATTGTTGGGCATTGAG	6909
	CTCAATGCCCAACAATCCGATCTGTTCTGATAGGTGAAGGTGAAA TTCTTCTCAGATTTCAATTGGTGGCGCAAACGGAAGAAGACCCTAT TCTGGGCTTTGGGTATATTCTTGGTAGTG	6910

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA	CACCAATTGAAATCTGA	6911
	TCAGATTTCAATTGGTG	6912
	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA CCAATTTAAATCTGTGAAGAATTTACCTTCACCTATACGAACAGAT CGGAATTGTTGGGCATTGAGGGTAAGTG	6913
	CACTTACCCTCAATGCCCAACAATTCCGATCTGTTCTGATAGGTGA AGGTGAAATCTTCAACAGATTTAAATTGGTGGCGCAAACGGAAGAA GACCTATTCTGGGCTTTGGGTATATTCT	6914
	TAAATCTGTGAAGAATT	6915
	AATTCTTCAACAGATTTA	6916
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTGTGAGTTCTGAGTCACC TATGGCAAGTTGAGTGATTTGAGAATGTGGGCTAAGGCCACTTCC AAGAATCTATGCCAGGCCCAGAAGTGGA	6917
	TCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCC ACATTCTGAAATCACTCAACTTGCCATAGGTGACTCAGAACTCAAA AAAAACAAAGAAGAGGAGGATAATAAAGAG	6918
	GCAAGTTGAGTGATTTT	6919
	GAAATCACTCAACTTGC	6920
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA	TATCCTCCTCTTCTTTGTTTTTTTGTGAGTTCTGAGTCACCTATGGCA AGTTGGGTGATTTGAGAATGTGGGCTAAGGCCACTTCCAAGAATC TATGCCAGGCCCAGAAGTGAGCTTCATG	6921
	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGC CTTAGCCACATTCTCAAATCACCCAACCTTGCCATAGGTGACTCAG AACTCAAAAAAAAAACAAAGAAGAGGAGGATA	6922
	GGTGATTTGAGAATGTG	6923
	CACATTCTCAAATCACC	6924
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA	TCCTCCTCTTCTTTGTTTTTTTGTGAGTTCTGAGTCACCTATGGCAAG TTGGGTGATTTCAATAATGTGGGCTAAGGCCACTTCCAAGAATCTAT GCCAGGCCCAGAAGTGAGCTTCATGTT	6925
	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTG GCCTTAGCCACATTATGAAATCACCCAACCTTGCCATAGGTGACTC AGAACTCAAAAAAAAAACAAAGAAGAGGAGGA	6926
	TGATTTCAATAATGTGGG	6927
	CCCACATTATGAAATCA	6928

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO.
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA	CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTTCAAGATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTTCAAC	6929
	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGA AGTGGCCTTAGCCCTCATTCTGAAATCACCCAACCTTGCCATAGGTG ACTCAGAACTCAAAAAAACAAAGAAGAG	6930
	TCAGAATGAGGGCTAAG	6931
	CTTAGCCCCCATTCTGA	6932
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGGTTTTCATGCTTAAGAAGAAGAAGAAGAGGATTTGCACTT AAGCAATCCTCCTCCATTCAATATTGGTC	6933
	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC TTCTTCTTCTTCTTAAGCATGAAAACCATTAACGCCATTAGAATTG GGGTGTCTTTGACTGTTGCTGCTTCAT	6934
	TTCATGCTTAAGAAGAA	6935
	TTCTTCTTAAGCATGAA	6936
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG GTTTTCATGCTAAATAAGAAGAAGAAGAAGAGGATTTGCACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	6937
	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTTAATTAGCATGAAAACCATTAACGCCATTAGAA TTGGGGTGTCTTTGACTGTTGCTGCTT	6938
	ATGCTAAATAAGAAGAA	6939
	TTCTTCTTAATTAGCAT	6940
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGCACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6941
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGACTGTTGCTG	6942
	CTAAAGAATAAGAAGAA	6943
	TTCTTCTTAATTCTTTAG	6944
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGCACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	6945
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGACTGTTGCTG	6946

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAAT <u>A</u> AAGAAGAA	6947
	TTCTTCTT <u>A</u> TTCTTTAG	6948
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTAG <u>G</u> TTTGATCCAAGTGCTCCACCACCCTTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAAA	6949
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGGA GCACTTGGATCAA <u>A</u> CTAAGCTTGATCTTCTTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTTGGACC	6950
	CAAGCTTAG <u>G</u> TTTGATCC	6951
	GGATCAA <u>A</u> CTAAGCTTG	6952
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGTG CTCCACCACCCTTCTAGATTGCAAATATCAGAGCAGCAATTCCAAA ACATTGCTGGGAGAAGAACACATTGAGAT	6953
	ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCT GATATTTGCAATCT <u>A</u> GAAGGGTGGTGGAGCACTTGGATCAAATAA GCTTGATCTTCTTTCCCTGCACCATTACC	6954
	CACCTTCTAGATTGCA	6955
	TGCAATCT <u>A</u> GAAGGGTG	6956
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA AGATTGCAAATATCTGAGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTTT	6957
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTT GGAATTGCTGCTC <u>A</u> GATATTTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAATAAGCTTGATCTTCTTT	6958
	CAAATATCTGAGCAGCA	6959
	TGCTGCTC <u>A</u> GATATTTG	6960
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA GAGCAGCAATTCCA <u>T</u> AACATTGCTGGGAGAAGAACACATTGAGATC TCTGAGTTATGTTCTGAGGGATGTGTTGG	6961
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTT <u>A</u> TGGAATTGCTGCTCTGATATTTGCAATCTTG AAGGGTGGTGGAGCACTTGGATCAAATA	6962
	CAATTCCAT <u>A</u> AACATTGC	6963
	GCAATGTT <u>A</u> TGGAATTG	6964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGC CCGGCTCGTGCTCTCCTAGTGCTCGGGCCTCGCGCCCGTCCGCC GCCTGCGCGCCGGCCGGGGCGCCATTGCGGGCGC	6965
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGGGACGG GCGCGAGGCCCGAGCACTAGGAGAGCACGAGCCGGGCCATTGC CGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	6966
	TGCTCTCCTAGTGCTCG	6967
	CGAGCACTAGGAGAGCA	6968
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGCCCGG CTCGTGCTCTCCGAGTGATCGGGCCTCGCGCCCGTCCGCCGCCT GCGCGCCGGCCGGGGCGCCATTGCGGGCGGGTCA	6969
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGGCGG ACGGGCGCGAGGCCCGATCACTCGGAGAGCACGAGCCGGGCCA TTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	6970
	TCCGAGTGATCGGGCCT	6971
	AGGCCCGATCACTCGGA	6972
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG	CCGCACCCGCACCCGCCCGCTGACGGCGGCAATGGCCCGGCT CGTGCTCTCCGAGTGCTAGGGCCTCGCGCCCGTCCGCCGCCTGC GCGCCGGCCGGGGCGCCATTGCGGGCGGGTACC	6973
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGC GGACGGGCGCGAGGCCCTAGCACTCGGAGAGCACGAGCCGGGC CATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	6974
	CGAGTGCTAGGGCCTCG	6975
	CGAGGCCCTAGCACTCG	6976
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA	GCTCGGGCCTCGCGCCCGTCCGCCGCTGCGCGCCGGCCGGGG CGCCATTGCGGGCGGGTGACCCCCCGCGCTCTCCGCGGCGCCG CGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	6977
	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCG CGGAGAGCGCGGGGGGTACCGCGCCGCAATGGCGCCCCGGCC GGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	6978
	GGCGCGGTGACCCCCG	6979
	CGGGGGGTACCGCGCC	6980
25 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG	CCCCCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC CCCCGCAATGAGGCCGTAGCAGGAGGCGAGCTGCAAGGCCACC GAGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	6981
	GCTTGGCGGCGTCAACTCGGAGCGGTGGTCCTCGGTGGCCTTG CAGCTCGCCTCCTGCTACGGCCTCATTGCGGGGGCCATGGCCGC GGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG	6982

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCG <u>T</u> AGCAGGAG	6983
	CTCCTGCT <u>A</u> CGGCCTCA	6984
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG	CCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCC CGCAATGAGGCCGGAGTAGGAGGCGAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	6985
	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGC CTTGACAGCTCGCCTCCT <u>A</u> CTCCGGCCTCATTGCGGGGGCCATGG CCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	6986
	GGCCGGAGTAGGAGGCG	6987
	CGCCTCCT <u>A</u> CTCCGGCC	6988
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG	CCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGC AATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	6989
	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGT GGCCTTGACAGCTCGCCT <u>A</u> CTGCTCCGGCCTCATTGCGGGGGCCA TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	6990
	CGGAGCAGTAGGCGAGC	6991
	GCTCGCCT <u>A</u> CTGCTCCG	6992
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCGAGCTG <u>A</u> AAGGCCACCGAGGACCACCGCTCCGA GTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	6993
	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGG TGGTCCTCGGTGGCCTT <u>T</u> CAGCTCGCCTCCTGCTCCGGCCTCATT GCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	6994
	GCGAGCTG <u>A</u> AAGGCCAC	6995
	GTGGCCTT <u>T</u> CAGCTCGC	6996
20 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Ser4Term TCG-TAG	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGG CGGCAATGGCGGCGT <u>A</u> GGCGACCCAGGAGGCCGACTGCAAGGC TTCCGAGGACGCCCGTCTCTTCTTCGACGCCGC	6997
	GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGACGTC GGCCTCCTGGGTGCGCT <u>A</u> CGCCGCCATTGCCGCCGGGGTGTGCT GGTGGATCTGATTCCGATTTGTGATTTGTGAAG	6998
	GGCGGCGT <u>A</u> GGCGACCC	6999
	GGGTCGCC <u>T</u> ACGCCGCC	7000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
5 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCGACTGCAAGGCTTCCGAGG ACGCCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	7001
	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAAGTCGGCCTCCTAGGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	7002
	CGGCGACCTAGGAGGCC	7003
	GGCCTCCTAGGTCGCCG	7004
10 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	7005
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAAGTCGGCCTACTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTGTCGTGGTGGATCTGATTCCGATTTGT	7006
	CGACCCAGTAGGCCGAC	7007
	GTCGGCCTACTGGGTCG	7008
15 Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTGAAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	7009
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTTCAGTCGGCCTCCTGGGTGCCGACGC CGCCATTGCCGCCGGGGTGTGTCGTGGTGGATCTGA	7010
	GCCGACTGAAGGCTTC	7011
	GAAGCCTTTCAGTCGGC	7012

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.
2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.
3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.
4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.
5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.
6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.
7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 4341-7012 .
8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

18. The method of claim 17 in which the alteration is produced in a plant cell extract.
19. The method of claim 17 in which the alteration is produced in a cell.
20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

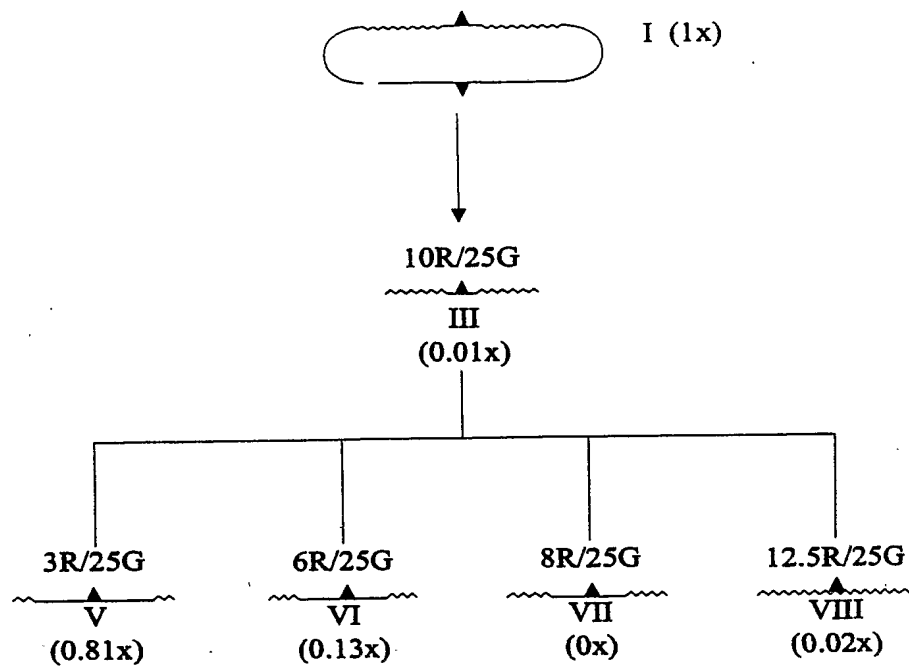


Figure 1A

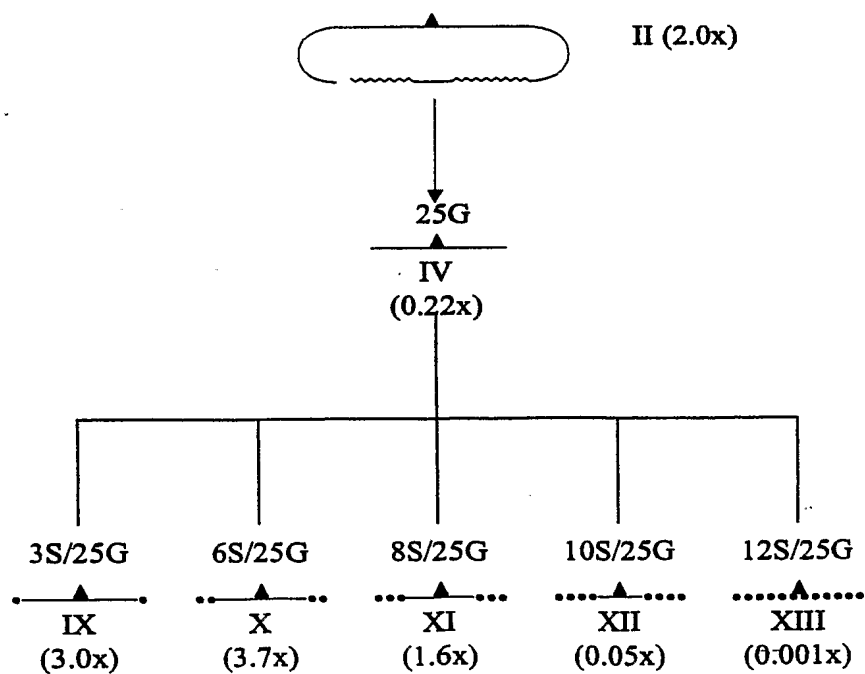


Figure 1B

Plasmids, DNA targets and chimeric oligonucleotides

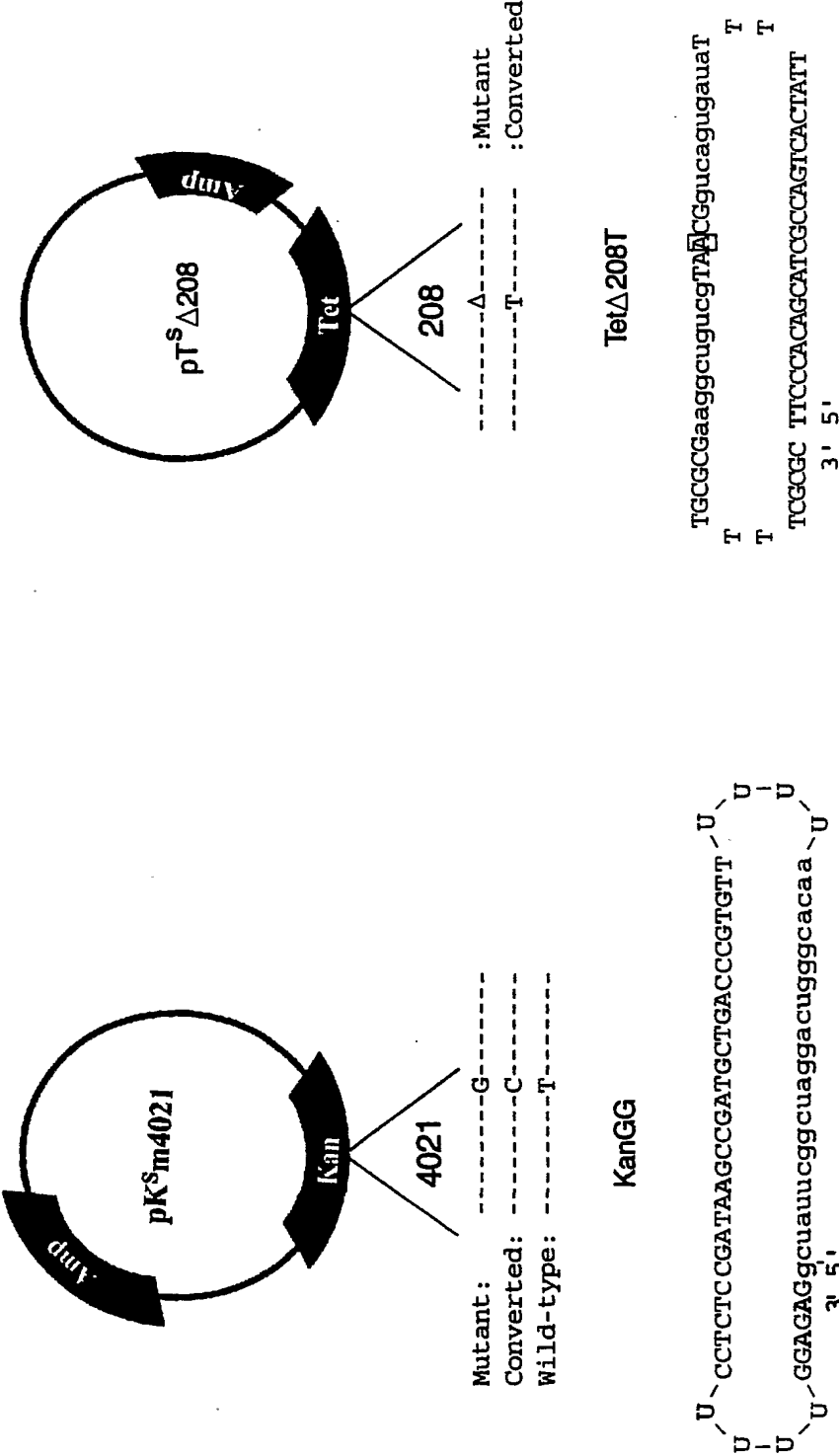
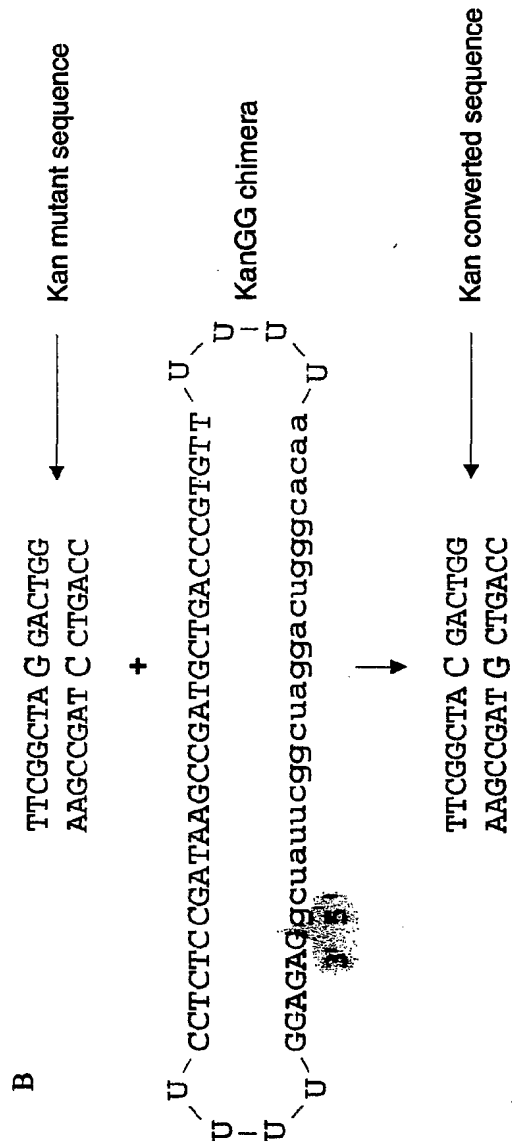


Figure 1C



DNA SEQUENCE ANALYSES

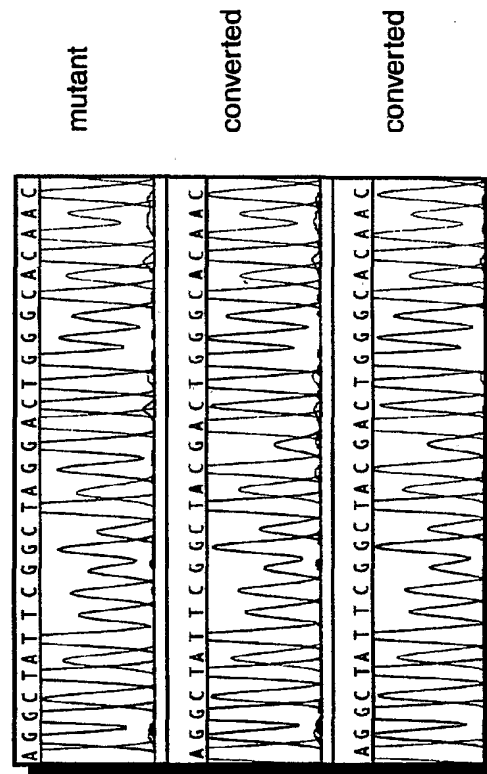


Figure 1D

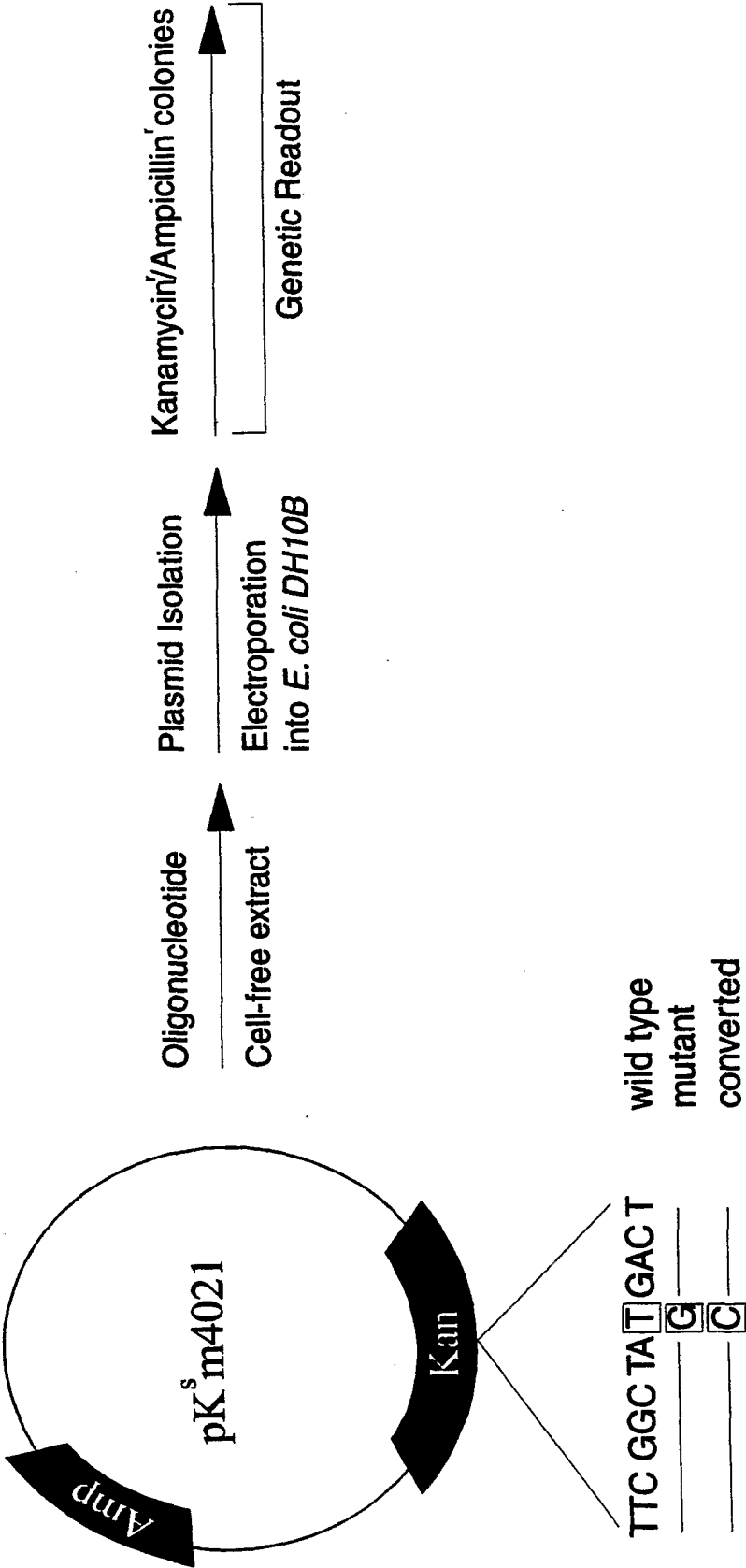
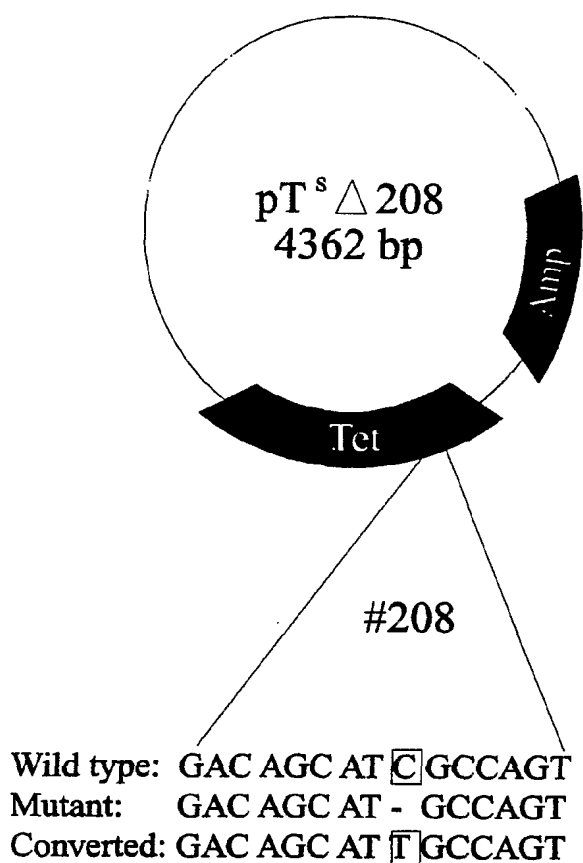


Figure 2



Sequence analysis of Tet^r plasmid $\Delta 208$

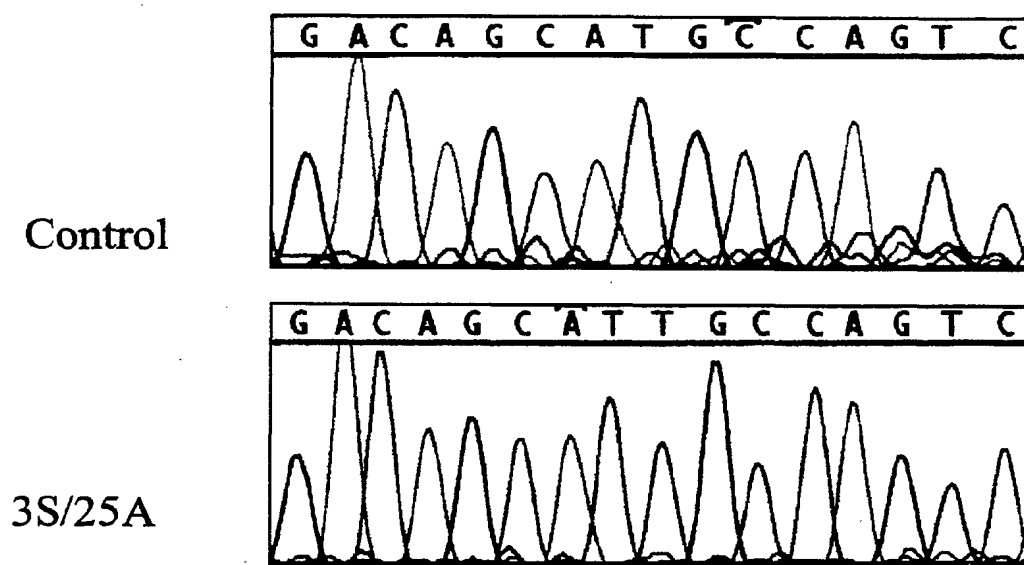


Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distribution					
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	----	+	---	---	---
2) 6S/25G (20)	----	+	---	---	---
3) 8S/25G (20)	----	+	---	---	---
4) 10S/25G (18)	----	+	---	+(2)	+(2)
5) 25S/25G (4)	---	---	+(2)	+(2)	---

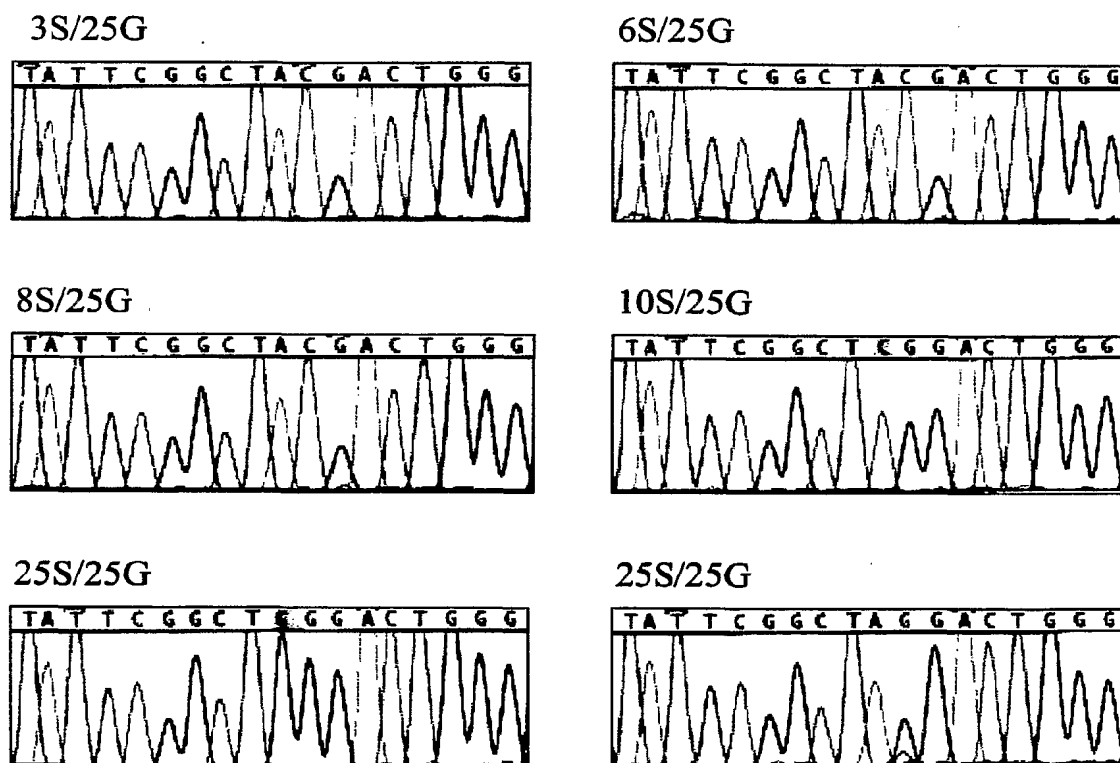


Figure 4

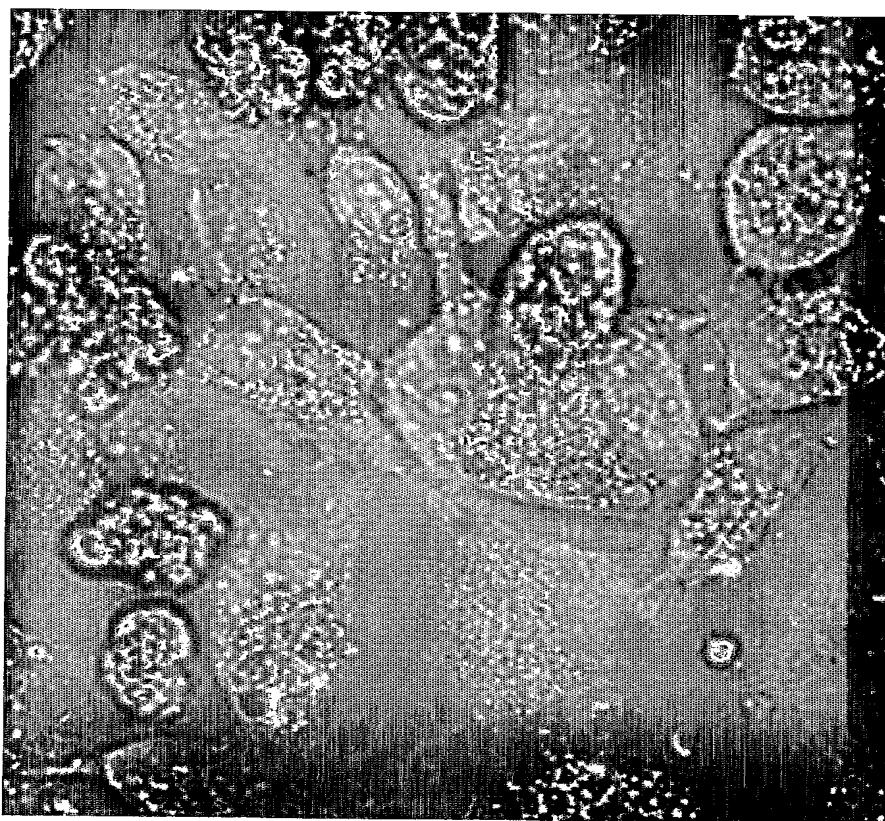


Figure 5

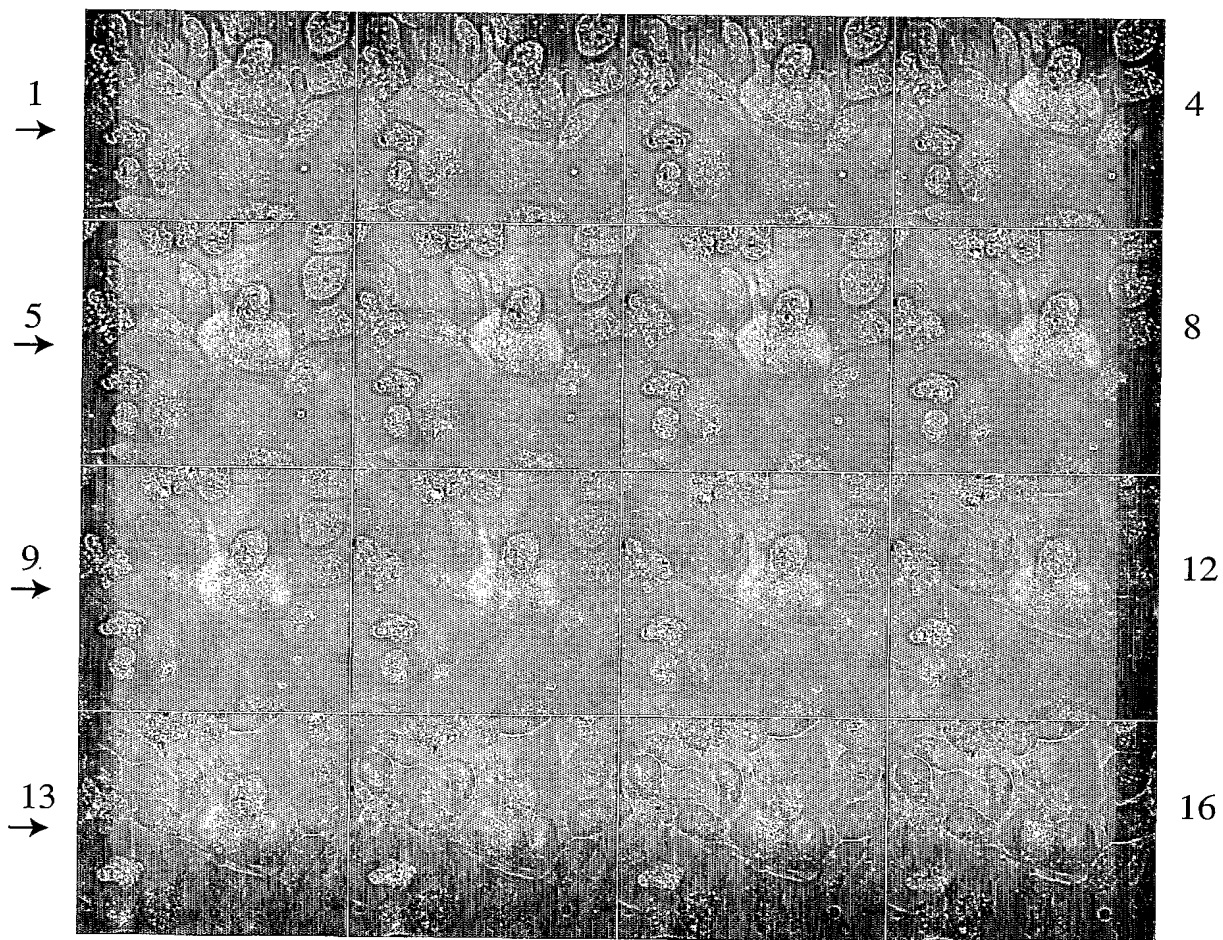
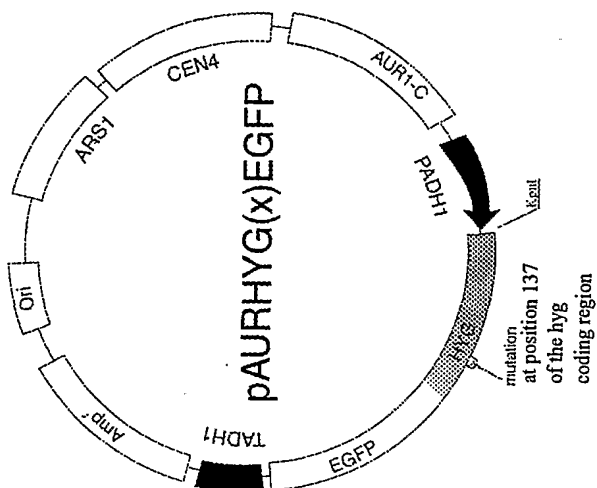


Figure 6

Sequence of normal allele: GTGGATATGTCCT
 Target/existing mutant: GTGGATAATGTCCT
 Desired alteration: GTGGATACGTCCT

Figure 7A



Sequence of normal allele: GTGGATATGTCCT
 Target/existing mutant: GTGGATAGGTCCT
 Desired alteration: GTGGATACGTCCT

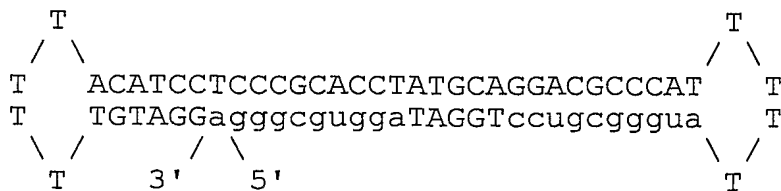
Figure 7B

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC
GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG
CCG ATG GTT TCT AC-3'

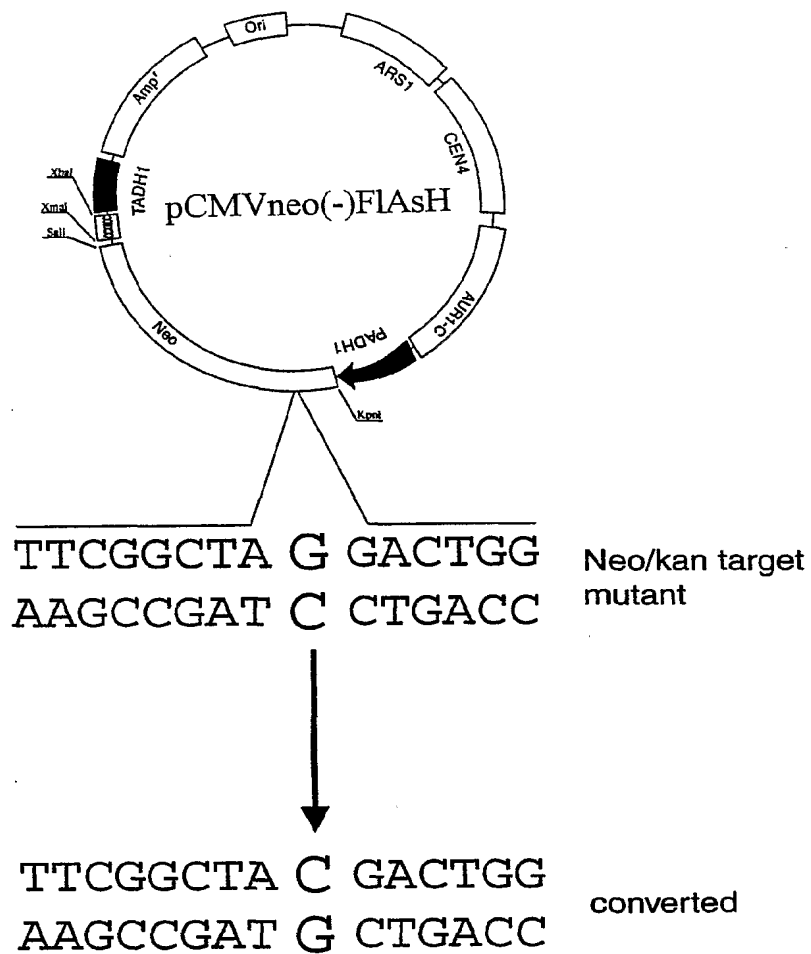
HygE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG
CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA
GCT GAA AGC ACG AG-3'

HygGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT
CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG
A-3'

Figure 8



FUSION GENE FOR LIGAND BINDING

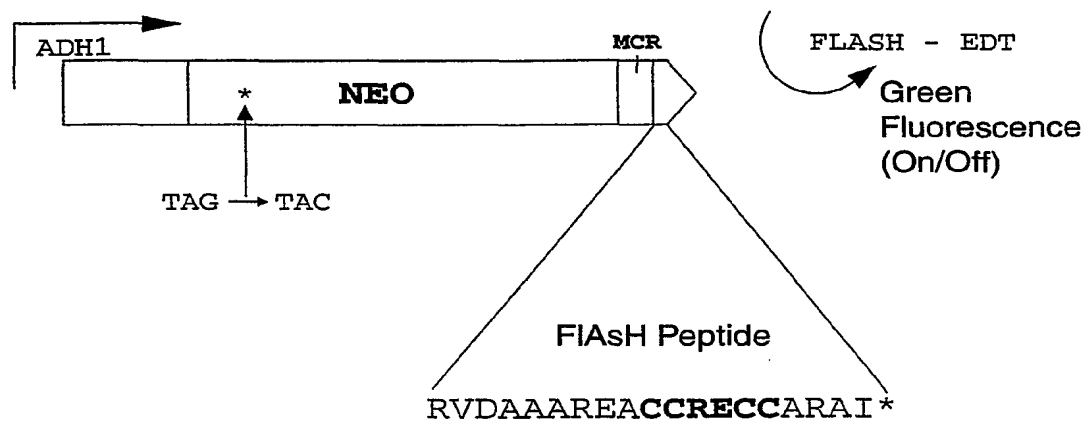


Figure 9

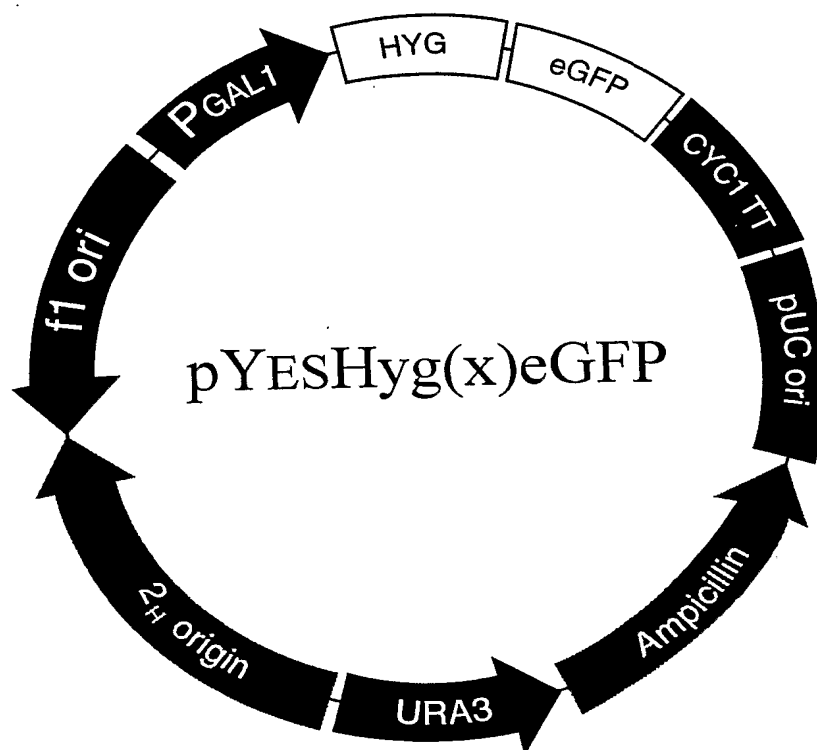


Figure 10

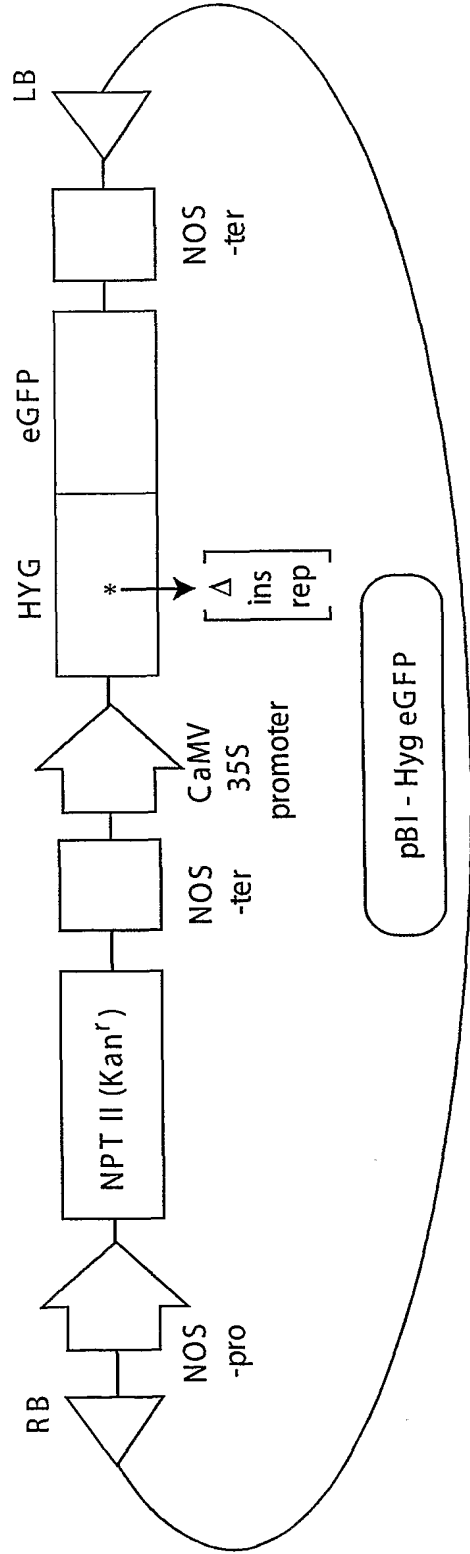


Figure 11